wwPDB EM Validation Summary Report

Jun 1, 2024 – 01:01 PM EDT

PDB ID	:	7U0H
EMDB ID	:	EMD-26259
Title	:	State NE1 nucleolar 60S ribosome biogenesis intermediate - Overall model
Authors	:	Cruz, V.E.; Sekulski, K.; Peddada, N.; Erzberger, J.P.
Deposited on	:	2022-02-18
Resolution	:	2.76 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (i)) were used in the production of this report:

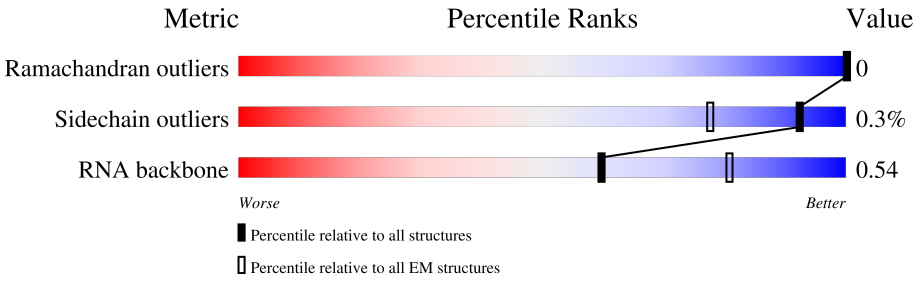
EMDB validation analysis	:	0.0.1.dev92
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 2.76 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	1	3396	18% 65% 14% 20%
2	2	158	11% 85% 15%
3	6	87	32% 44% 24% 32%
4	A	254	35% 69% 31%
5	B	387	88% 12%
6	C	362	7% 100%
7	E	176	11% 89% 11%
8	F	244	8% 91% 9%

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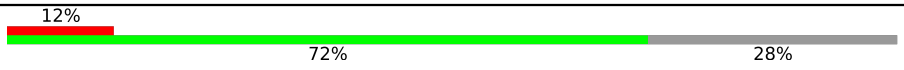
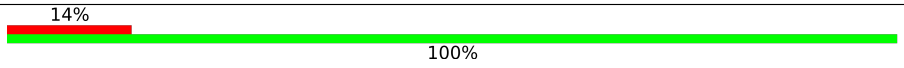
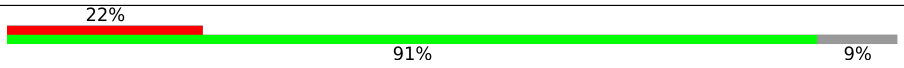
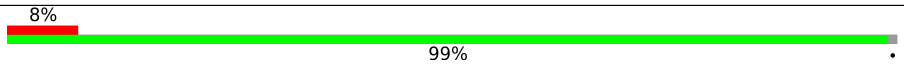
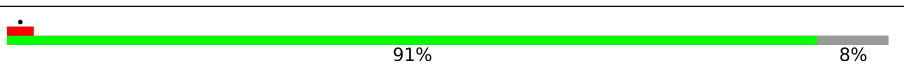
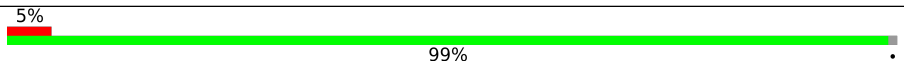
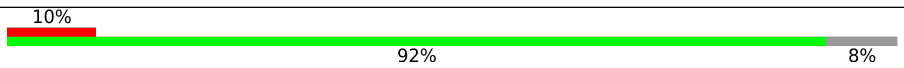
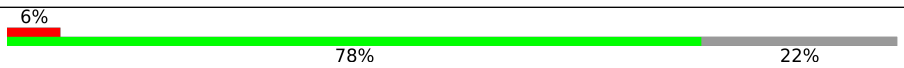
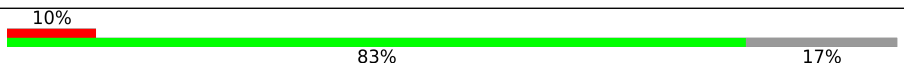
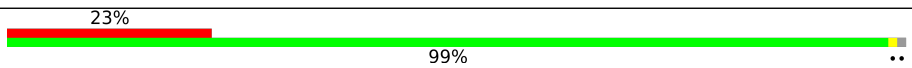
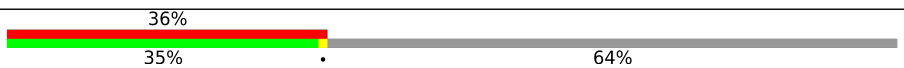
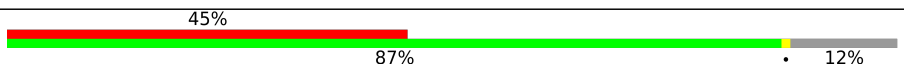
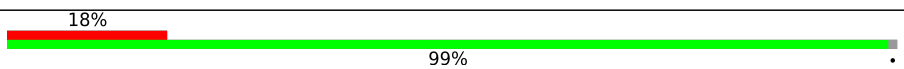
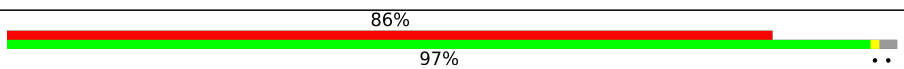
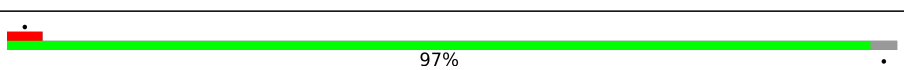
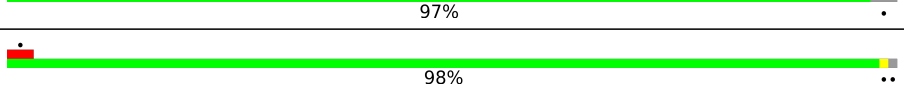
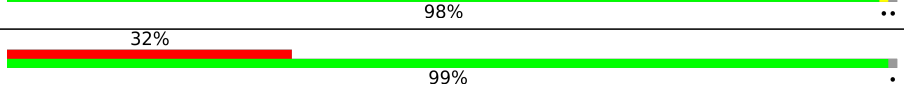
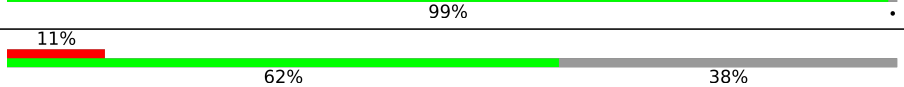
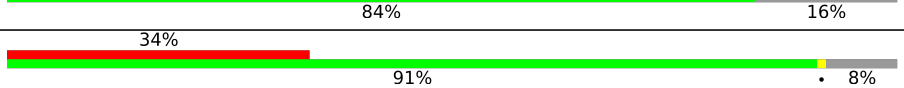
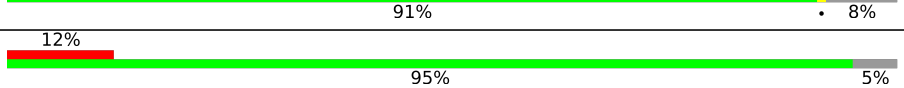
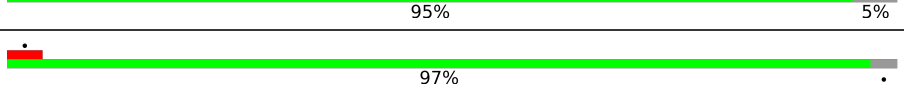
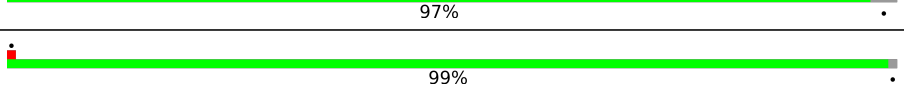
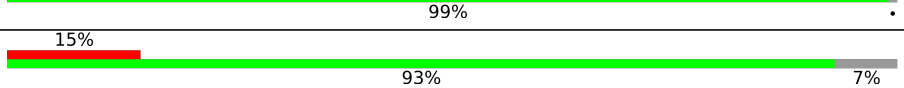
Mol	Chain	Length	Quality of chain
9	G	256	
10	H	191	
11	K	376	
12	L	199	
13	M	138	
14	N	204	
15	O	199	
16	P	184	
17	Q	186	
18	R	189	
19	S	172	
20	T	160	
21	U	121	
22	V	137	
23	W	236	
24	X	142	
25	Y	127	
26	Z	136	
27	a	149	
28	b	647	
29	c	105	
30	d	113	
31	e	130	
32	f	107	
33	g	121	

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Mol	Chain	Length	Quality of chain
34	h	120	8% 99%
35	i	100	44% 99%
36	j	88	17% 99%
37	k	78	28% 99%
38	m	9	100% 100%
39	n	605	21% 61% 39%
40	o	220	34% 60% 40%
41	p	92	32% 98%
42	q	455	35% 41% 58%
43	r	261	41% 63% 37%
44	s	520	7% 93%
45	t	322	50% 89% 11%
46	u	199	18% 71% 29%
47	w	841	31% 38% 62%
48	y	245	25% 99%
49	z	106	52% 52% 48%

2 Entry composition (i)

There are 51 unique types of molecules in this entry. The entry contains 124932 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	1	2722	58236	26005	10495	19014	2722	0	0

- Molecule 2 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	2	158	3353	1500	586	1109	158	0	0

- Molecule 3 is a RNA chain called ITS2 rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	6	59	1247	559	211	418	59	0	0

- Molecule 4 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
4	A	176	1356	856	263	237	0	0

- Molecule 5 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	B	340	2700	1713	502	479	6	0	0

- Molecule 6 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	C	361	2749	1730	522	494	3	0	0

- Molecule 7 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	E	156	Total	C	N	O	S	0	0
			1239	800	222	216	1		

- Molecule 8 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	F	222	Total	C	N	O	S	0	0
			1784	1151	324	308	1		

- Molecule 9 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	G	185	Total	C	N	O	S	0	0
			1470	948	258	262	2		

- Molecule 10 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	H	191	Total	C	N	O	S	0	0
			1518	963	274	277	4		

- Molecule 11 is a protein called Proteasome-interacting protein CIC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	256	Total	C	N	O	S	0	0
			2064	1332	342	387	3		

- Molecule 12 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	L	182	Total	C	N	O	0	0
			1459	907	300	252		

- Molecule 13 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	137	Total	C	N	O	S	0	0
			1059	678	200	179	2		

- Molecule 14 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	187	Total	C	N	O	S	0	0
			1604	1006	340	257	1		

- Molecule 15 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	197	Total	C	N	O	S	0	0
			1555	1003	289	262	1		

- Molecule 16 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	P	170	Total	C	N	O	0	0
			1341	833	265	243		

- Molecule 17 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	146	Total	C	N	O	S	0	0
			1132	716	218	197	1		

- Molecule 18 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	R	156	Total	C	N	O	0	0
			1258	781	265	212		

- Molecule 19 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	171	Total	C	N	O	S	0	0
			1437	925	266	243	3		

- Molecule 20 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	57	Total	C	N	O	S	0	0
			433	265	87	80	1		

- Molecule 21 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	U	106	Total 844	C 545	N 138	O 161	0	0

- Molecule 22 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	136	Total 1003	C 628	N 189	O 179	S 7	0	0

- Molecule 23 is a protein called Ribosome assembly factor MRT4.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	232	Total 1870	C 1184	N 321	O 360	S 5	0	0

- Molecule 24 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	X	138	Total 1082	C 694	N 193	O 193	S 2	0	0

- Molecule 25 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	Y	126	Total 993	C 625	N 192	O 176	0	0

- Molecule 26 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	Z	134	Total 1087	C 707	N 201	O 179	0	0

- Molecule 27 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	a	92	Total 731	C 477	N 129	O 124	S 1	0	0

- Molecule 28 is a protein called Nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	b	546	Total	C	N	O	S	0	0
			4430	2802	779	826	23		

- Molecule 29 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	c	97	Total	C	N	O	S	0	0
			743	479	124	139	1		

- Molecule 30 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	d	107	Total	C	N	O	S	0	0
			873	553	165	154	1		

- Molecule 31 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	e	126	Total	C	N	O	S	0	0
			1012	641	204	166	1		

- Molecule 32 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	f	106	Total	C	N	O	S	0	0
			850	540	165	144	1		

- Molecule 33 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	g	112	Total	C	N	O	S	0	0
			881	546	179	152	4		

- Molecule 34 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	h	119	Total	C	N	O	S	0	0
			969	615	186	167	1		

- Molecule 35 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	i	99	Total	C	N	O	S	0	0
			771	481	156	132	2		

- Molecule 36 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	j	87	Total	C	N	O	S	0	0
			681	414	148	114	5		

- Molecule 37 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms				AltConf	Trace
37	k	77	Total	C	N	O	0	0
			612	391	115	106		

- Molecule 38 is a protein called Nucleolar GTP-binding protein 2.

Mol	Chain	Residues	Atoms				AltConf	Trace
38	m	9	Total	C	N	O	0	0
			69	43	11	15		

- Molecule 39 is a protein called Pescadillo homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	n	368	Total	C	N	O	S	0	0
			3001	1944	519	528	10		

- Molecule 40 is a protein called Ribosome biogenesis protein 15.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	o	133	Total	C	N	O	S	0	0
			1107	716	198	189	4		

- Molecule 41 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	p	91	Total	C	N	O	S	0	0
			694	429	138	121	6		

- Molecule 42 is a protein called Ribosome biogenesis protein NOP53.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	q	189	Total	C	N	O	S	0	0
			1588	998	296	293	1		

- Molecule 43 is a protein called Ribosome biogenesis protein NSA2.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	r	164	Total	C	N	O	S	0	0
			1341	846	260	231	4		

- Molecule 44 is a protein called Nuclear GTP-binding protein NUG1.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	s	36	Total	C	N	O	S	0	0
			301	184	69	46	2		

- Molecule 45 is a protein called Ribosome biogenesis protein RLP7.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	t	287	Total	C	N	O	S	0	0
			2306	1459	427	417	3		

- Molecule 46 is a protein called Ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	u	141	Total	C	N	O	S	0	0
			1191	748	238	196	9		

- Molecule 47 is a protein called 27S pre-rRNA (guanosine(2922)-2'-O)-methyltransferase.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	w	321	Total	C	N	O	S	0	0
			2610	1629	480	485	16		

- Molecule 48 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	y	244	Total	C	N	O	S	0	0
			1849	1146	319	377	7		

- Molecule 49 is a protein called UPF0642 protein YBL028C.

Mol	Chain	Residues	Atoms				AltConf	Trace
49	z	55	Total	C	N	O	0	0
			444	273	88	83		

- Molecule 50 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
50	b	1	Total	Mg	0
			1	1	

- Molecule 51 is ZINC ION (three-letter code: ZN) (formula: Zn).

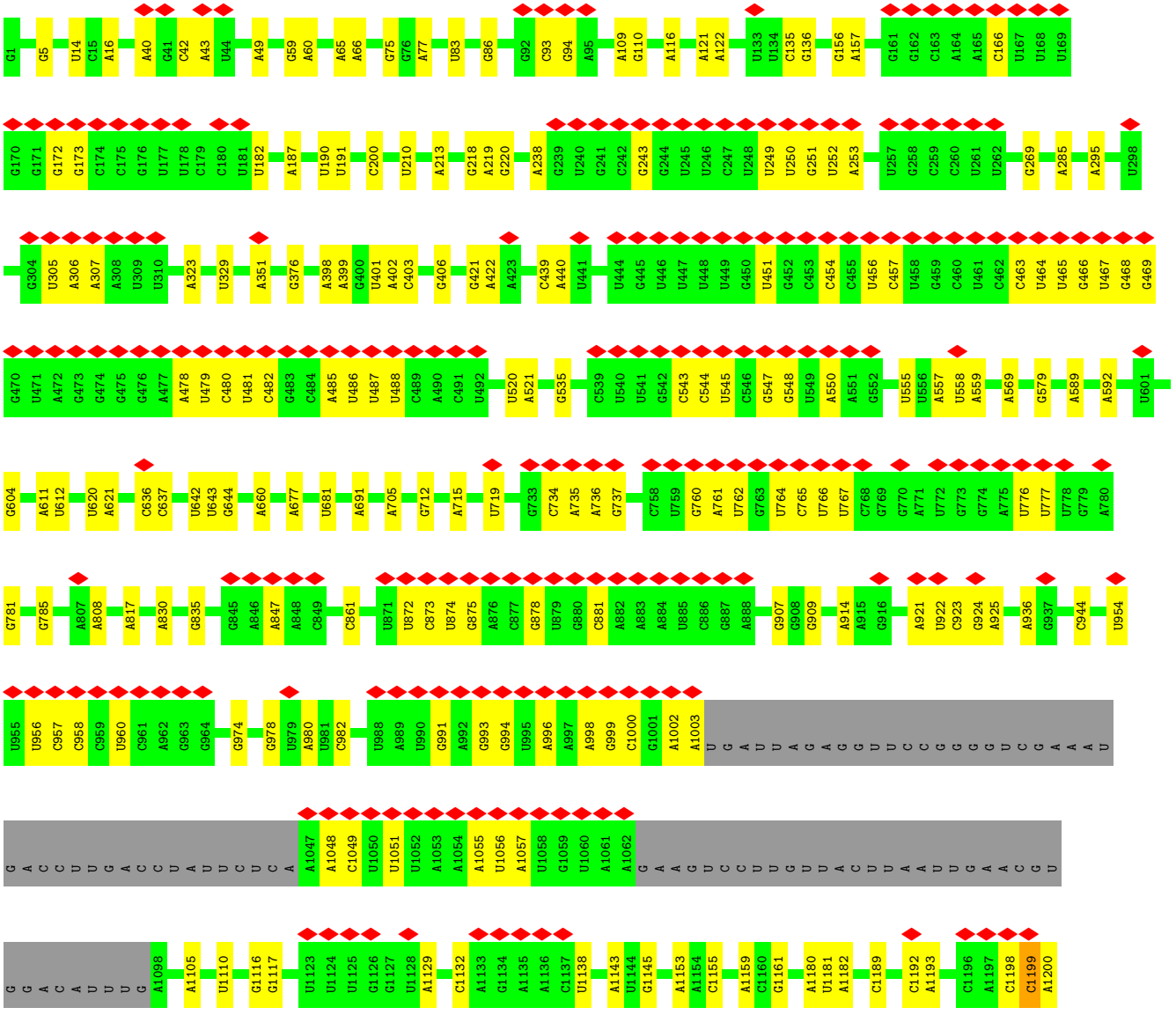
Mol	Chain	Residues	Atoms		AltConf
51	g	1	Total	Zn	0
			1	1	
51	j	1	Total	Zn	0
			1	1	
51	p	1	Total	Zn	0
			1	1	
51	u	1	Total	Zn	0
			1	1	

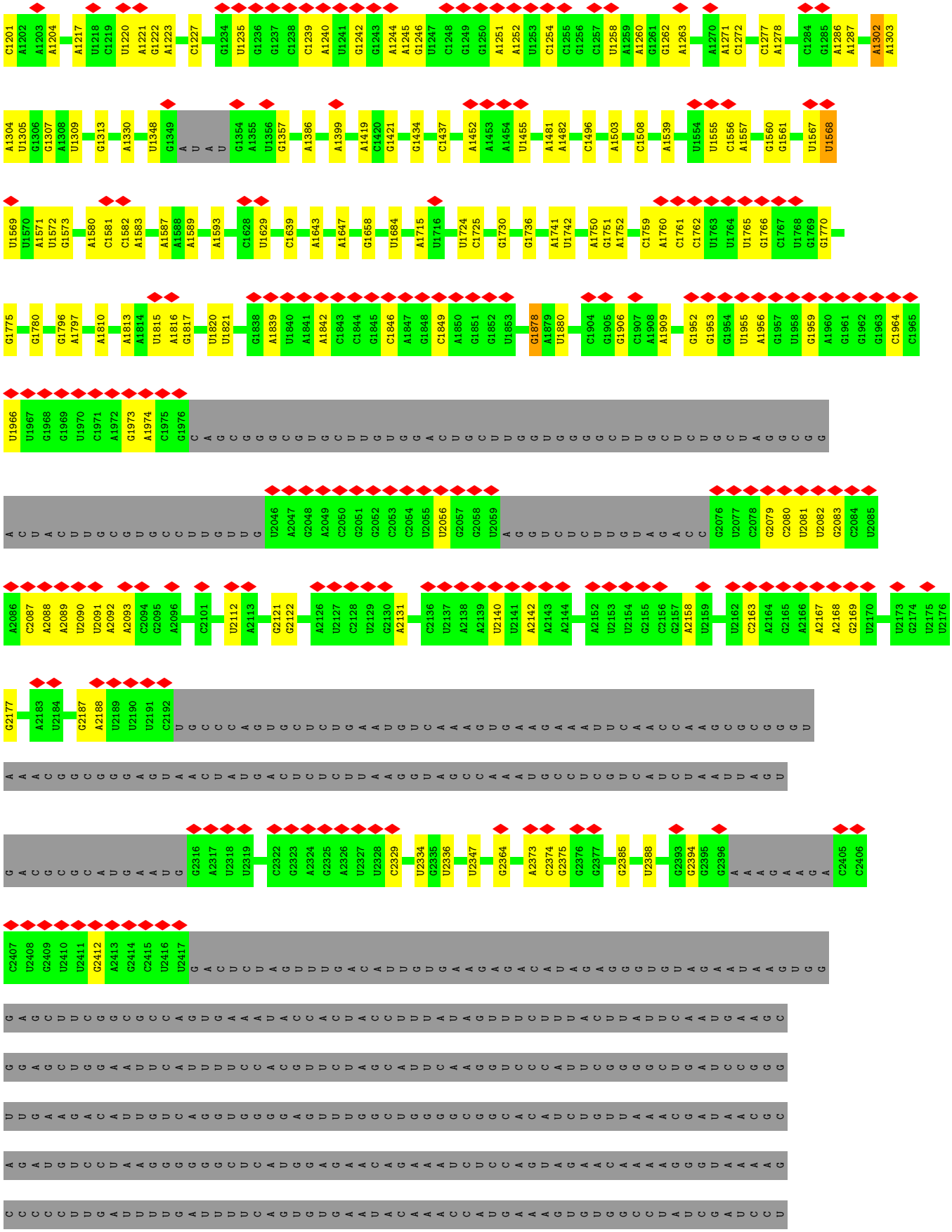
3 Residue-property plots (i)

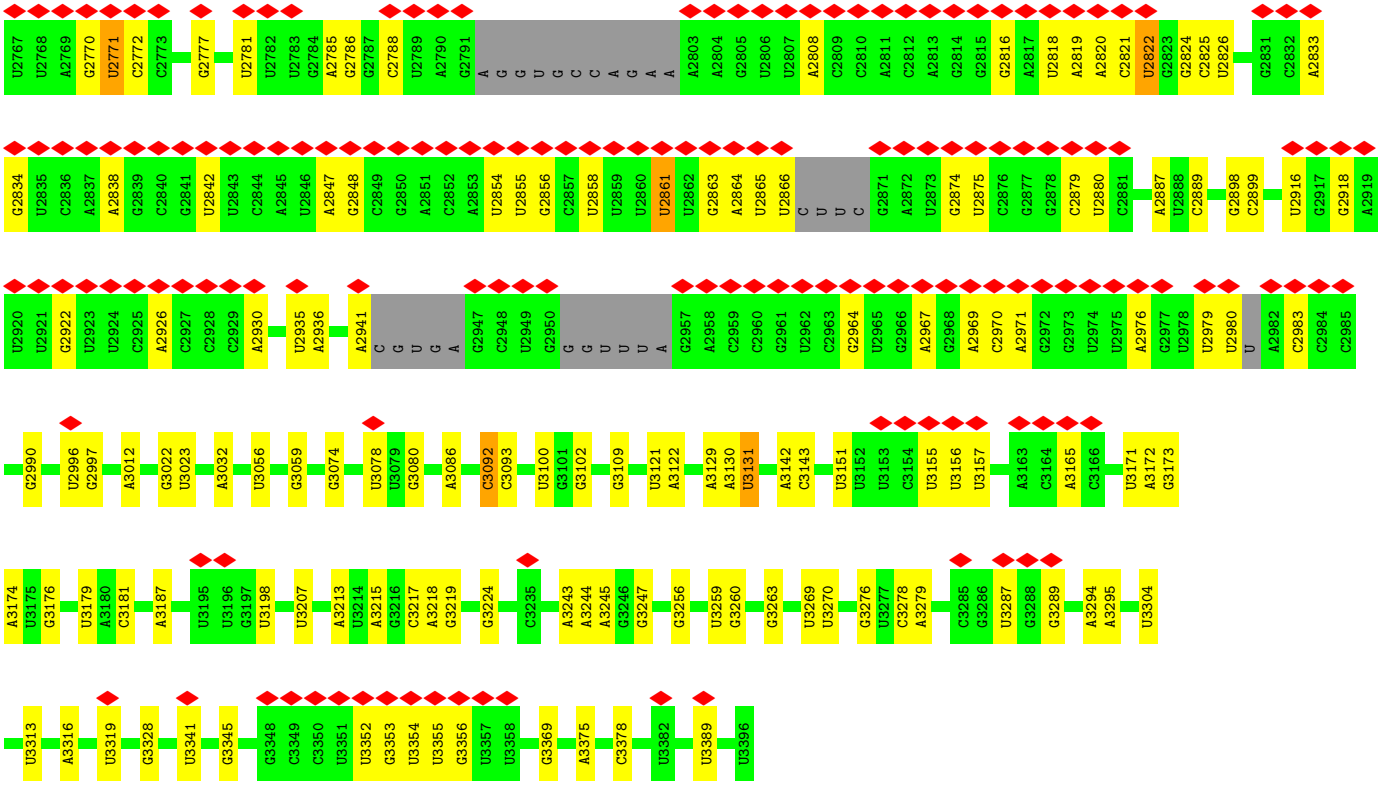
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: 25S rRNA

Chain 1:

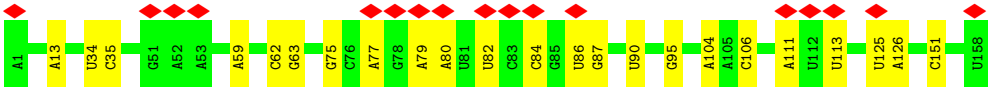






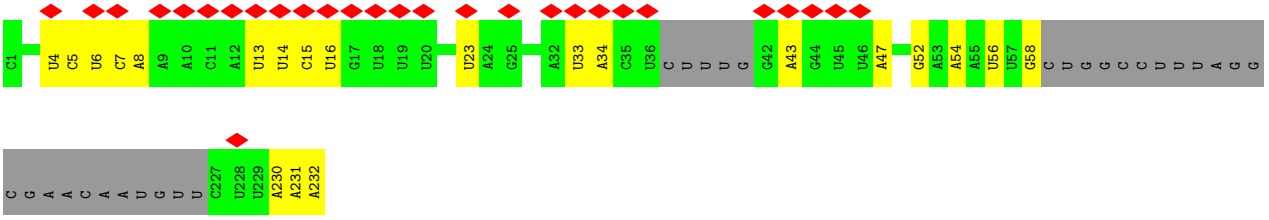
• Molecule 2: 5.8S rRNA

Chain 2:



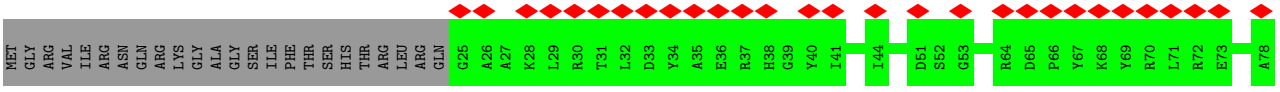
• Molecule 3: ITS2 rRNA

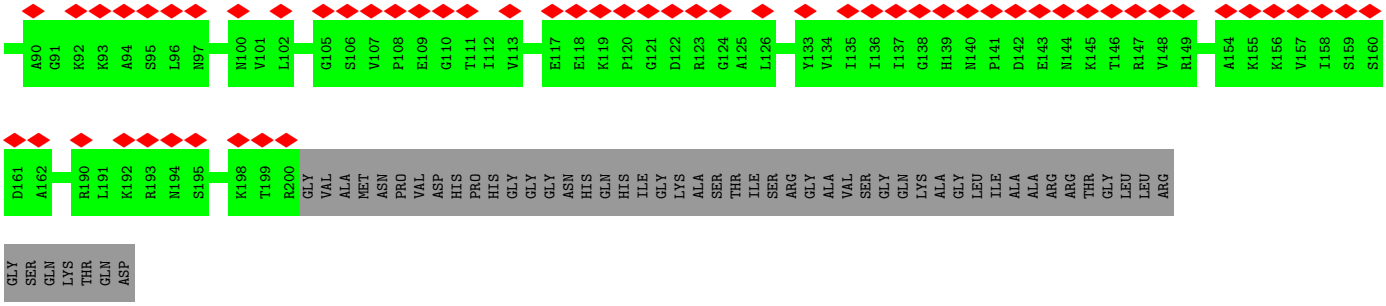
Chain 6:



• Molecule 4: 60S ribosomal protein L2-A

Chain A:



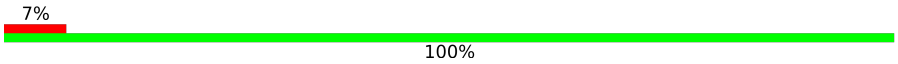


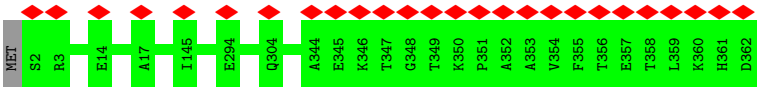
• Molecule 5: 60S ribosomal protein L3

Chain B:

• Molecule 6: 60S ribosomal protein L4-A

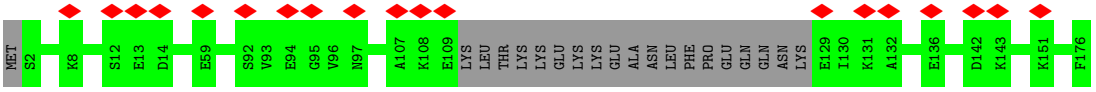
Chain C:





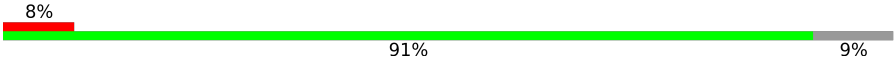
• Molecule 7: 60S ribosomal protein L6-A

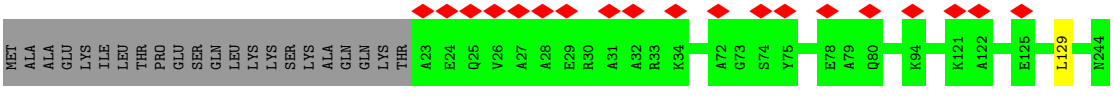
Chain E:



• Molecule 8: 60S ribosomal protein L7-A

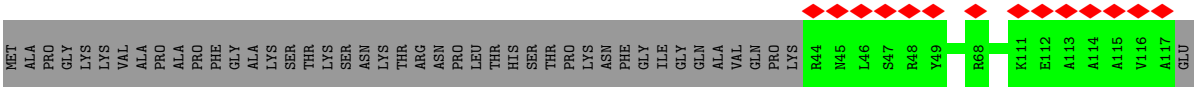
Chain F:

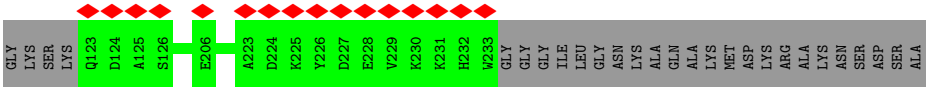




• Molecule 9: 60S ribosomal protein L8-A

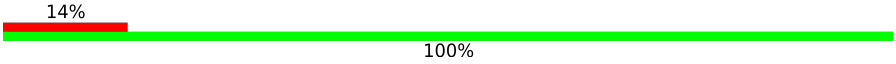
Chain G:

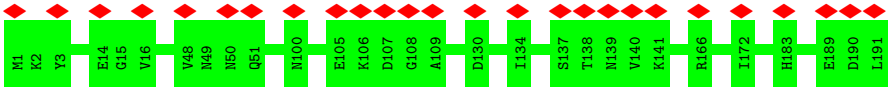




• Molecule 10: 60S ribosomal protein L9-A

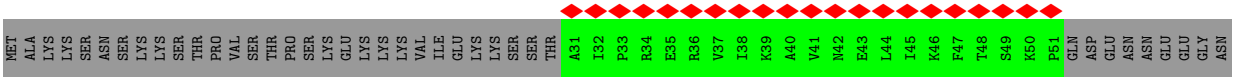
Chain H:

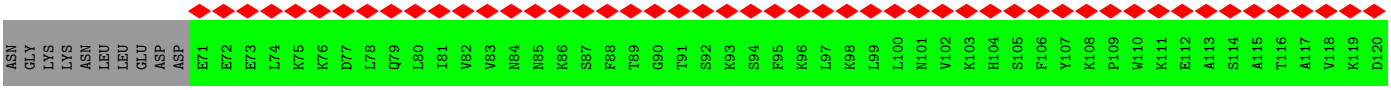


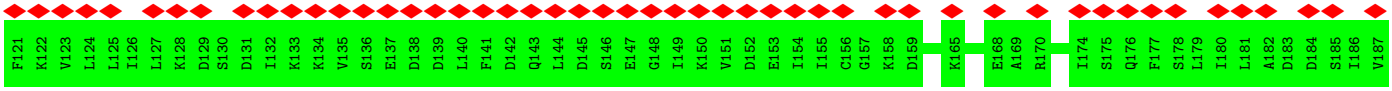


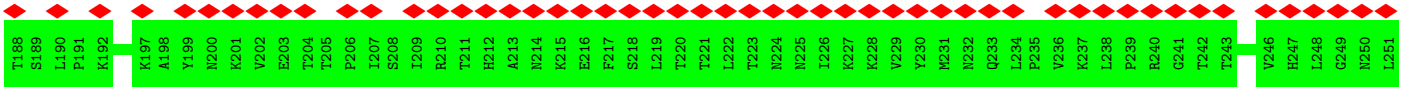
• Molecule 11: Proteasome-interacting protein CIC1

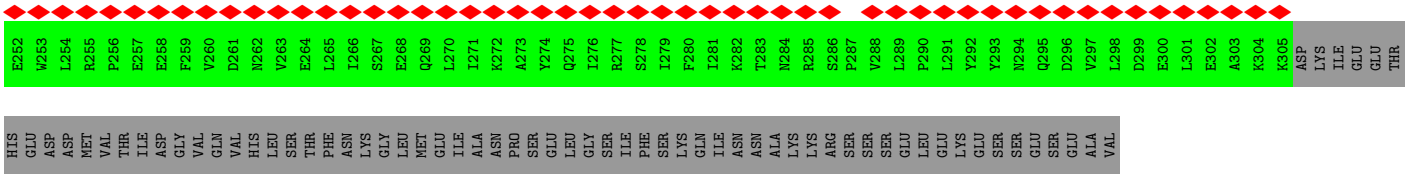
Chain K:





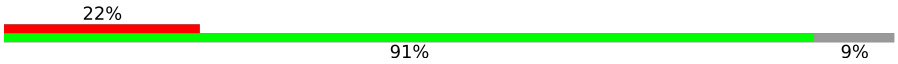


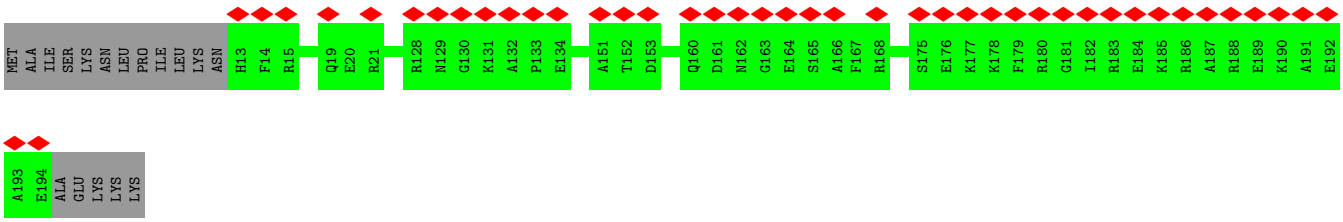




• Molecule 12: 60S ribosomal protein L13-A

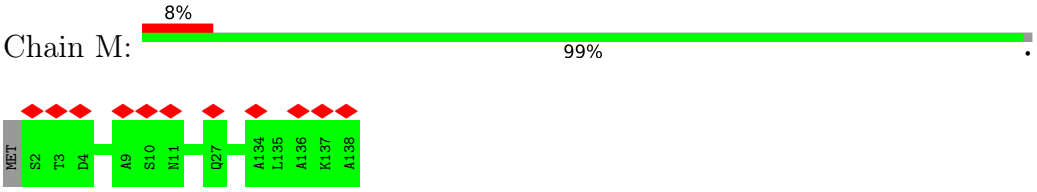
Chain L:





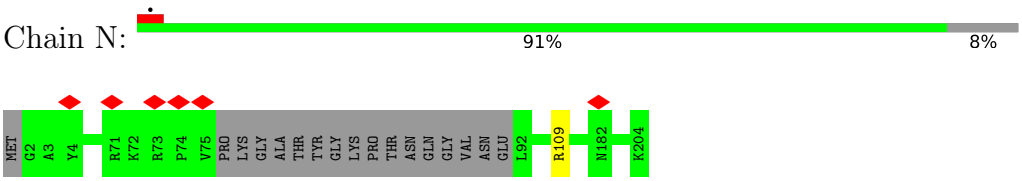
• Molecule 13: 60S ribosomal protein L14-A

Chain M:



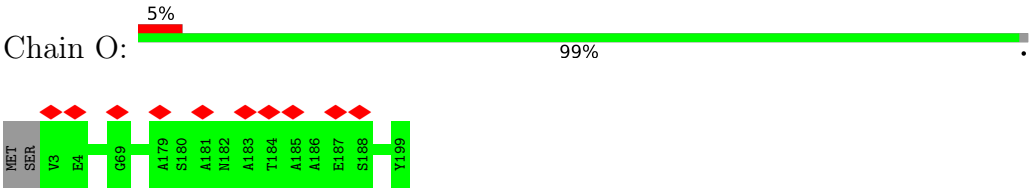
• Molecule 14: 60S ribosomal protein L15-A

Chain N:



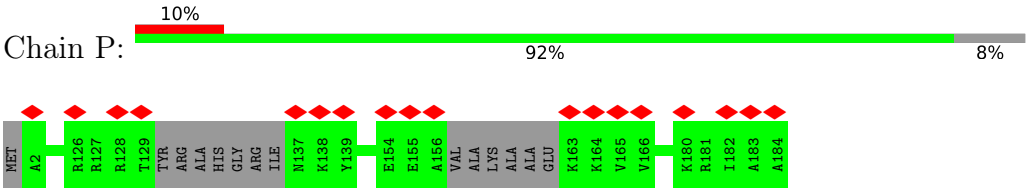
• Molecule 15: 60S ribosomal protein L16-A

Chain O:



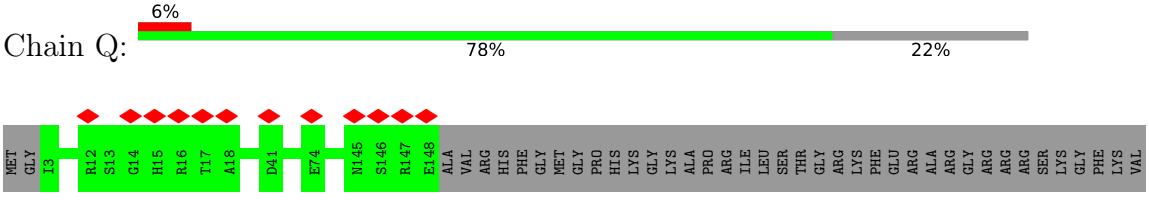
• Molecule 16: 60S ribosomal protein L17-A

Chain P:



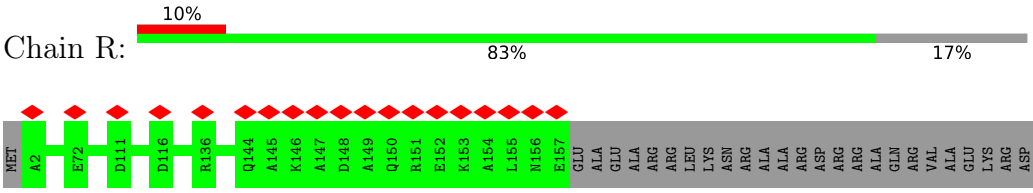
• Molecule 17: 60S ribosomal protein L18-A

Chain Q:



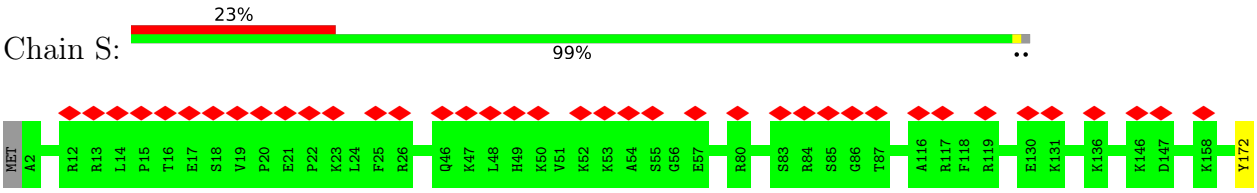
• Molecule 18: 60S ribosomal protein L19-A

Chain R:



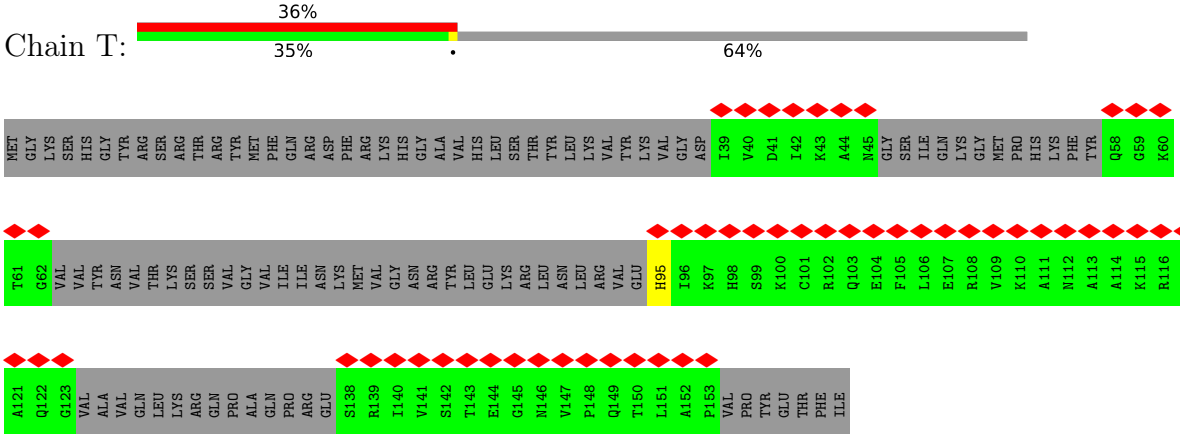
• Molecule 19: 60S ribosomal protein L20-A

Chain S:



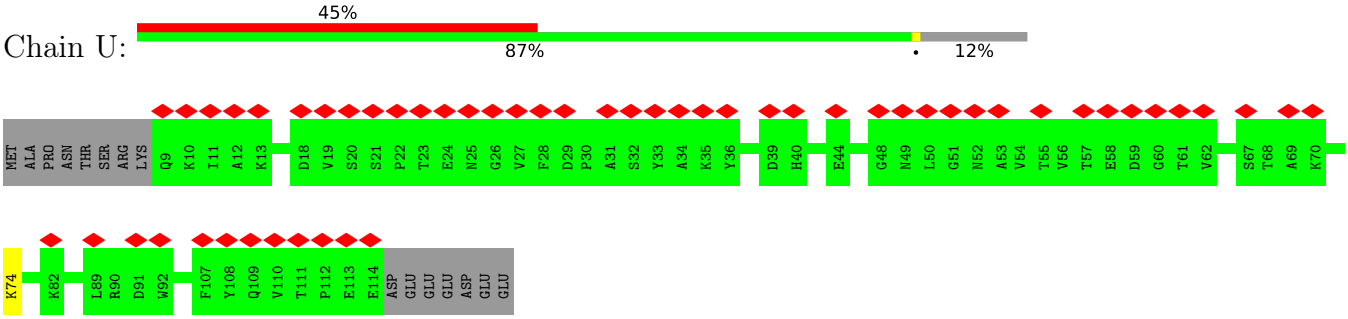
• Molecule 20: 60S ribosomal protein L21-A

Chain T:



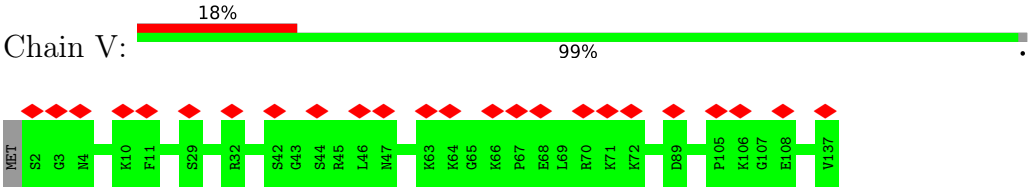
• Molecule 21: 60S ribosomal protein L22-A

Chain U:



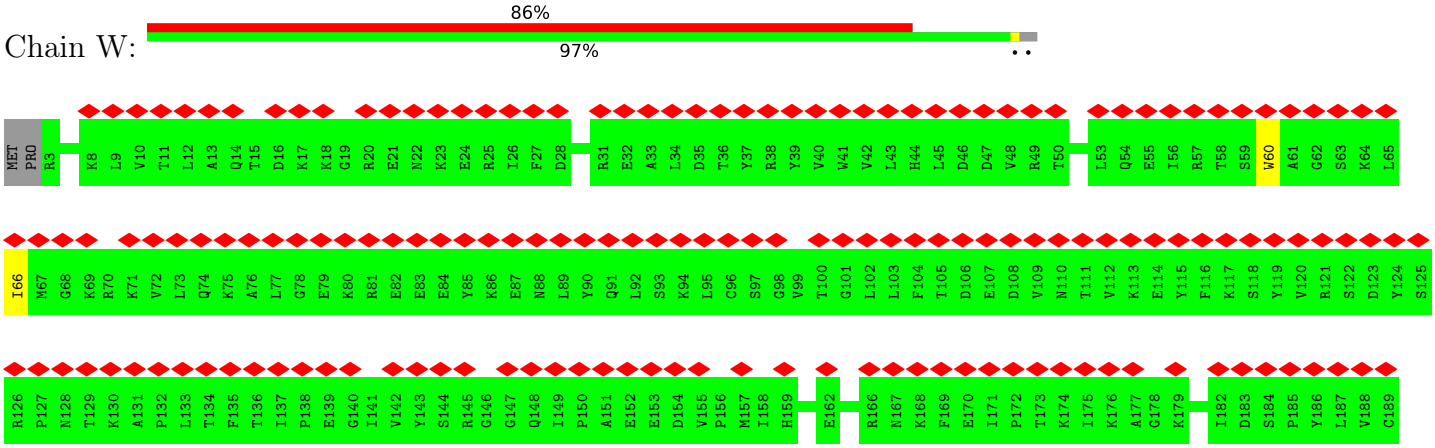
• Molecule 22: 60S ribosomal protein L23-A

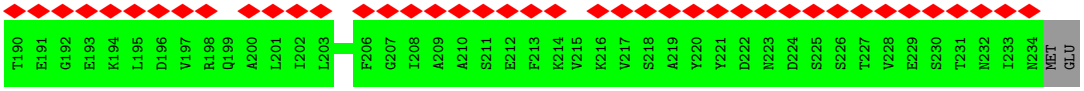
Chain V:



• Molecule 23: Ribosome assembly factor MRT4

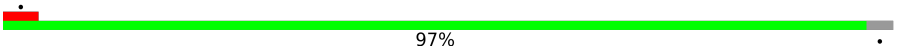
Chain W:

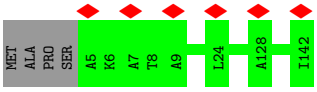




• Molecule 24: 60S ribosomal protein L25

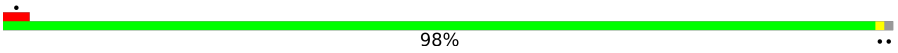
Chain X:

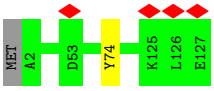




• Molecule 25: 60S ribosomal protein L26-A

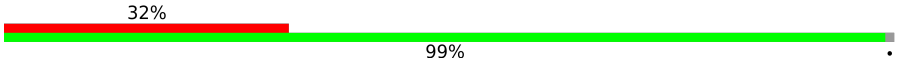
Chain Y:

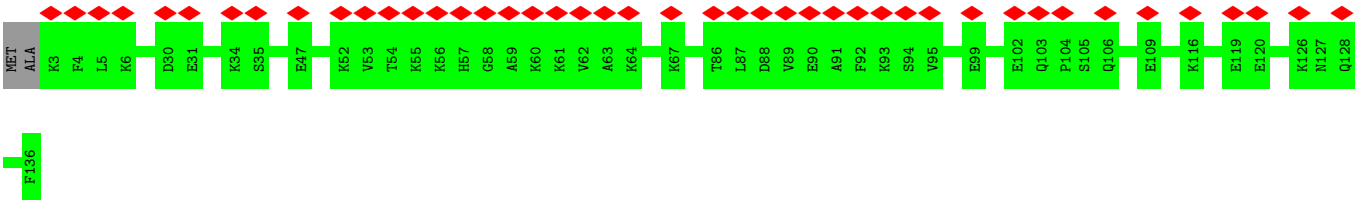




• Molecule 26: 60S ribosomal protein L27-A

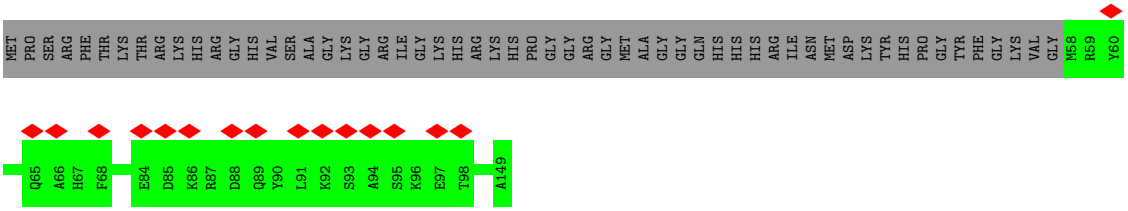
Chain Z:





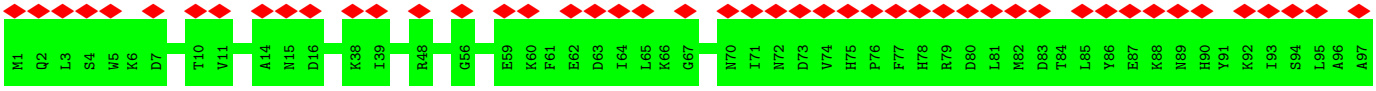
• Molecule 27: 60S ribosomal protein L28

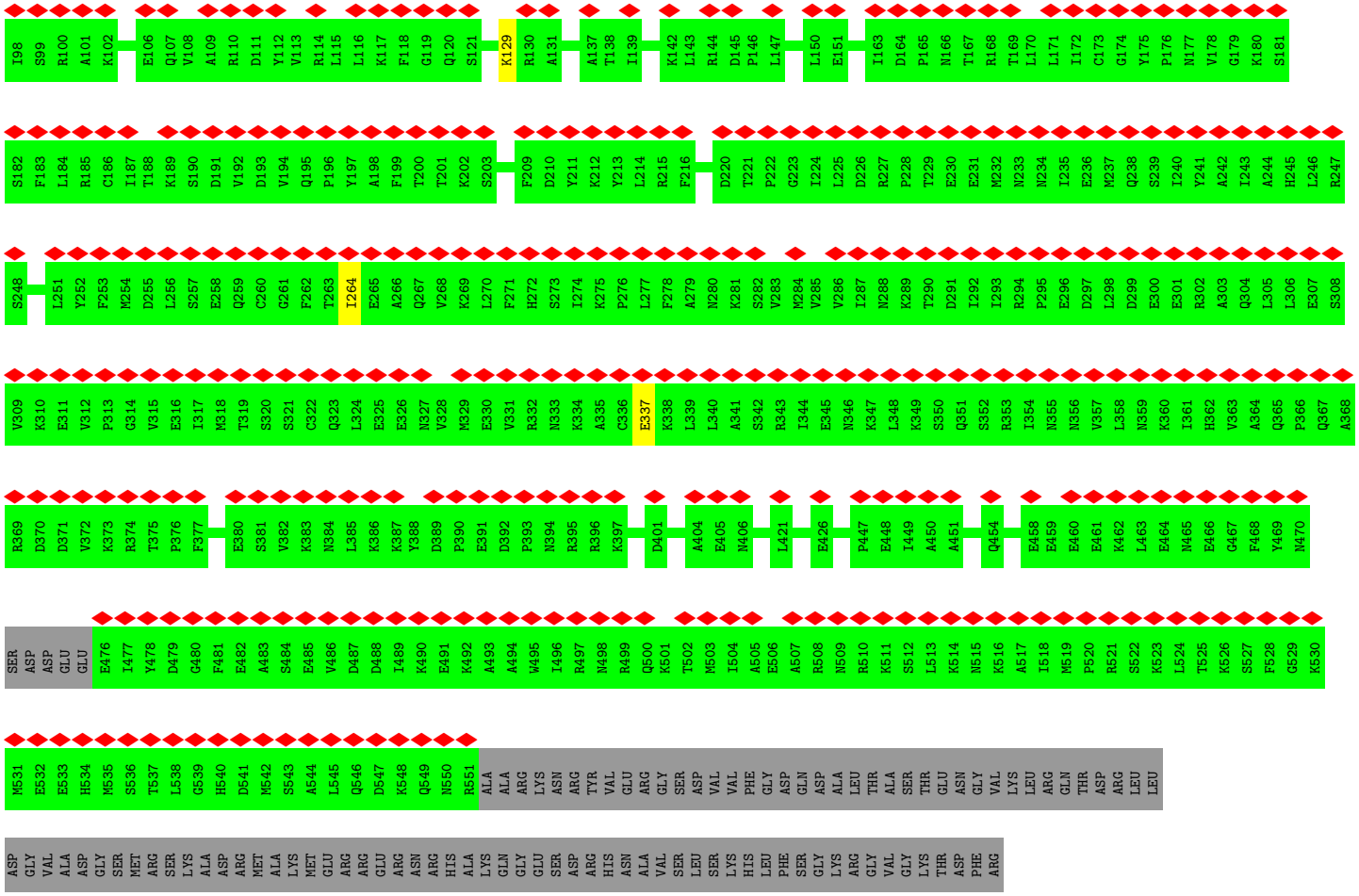
Chain a:



• Molecule 28: Nucleolar GTP-binding protein 1

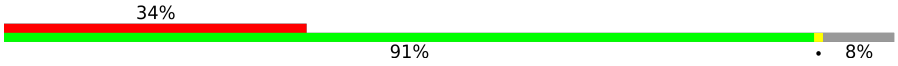
Chain b:

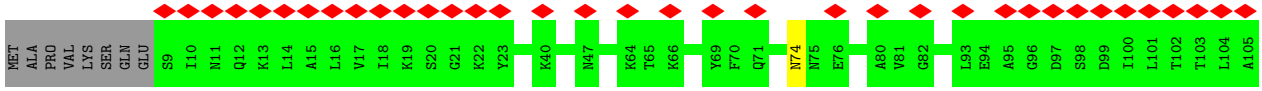




• Molecule 29: 60S ribosomal protein L30

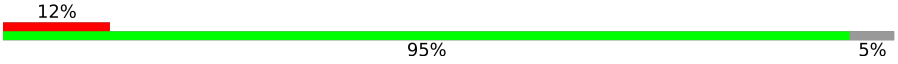
Chain c:

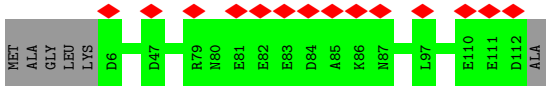




• Molecule 30: 60S ribosomal protein L31-A

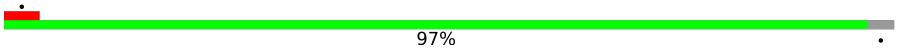
Chain d:

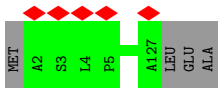




• Molecule 31: 60S ribosomal protein L32

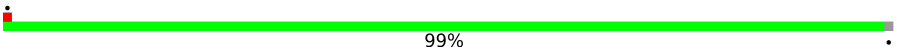
Chain e:





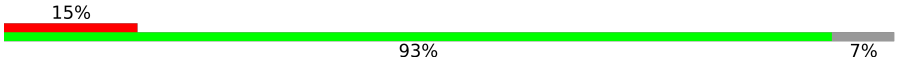
• Molecule 32: 60S ribosomal protein L33-A

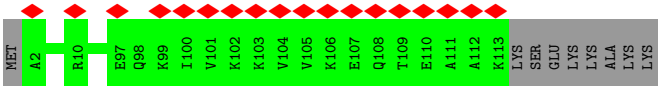
Chain f:



• Molecule 33: 60S ribosomal protein L34-A

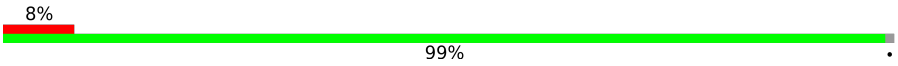
Chain g:

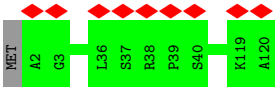




• Molecule 34: 60S ribosomal protein L35-A

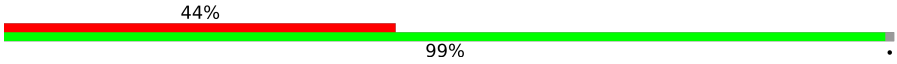
Chain h:

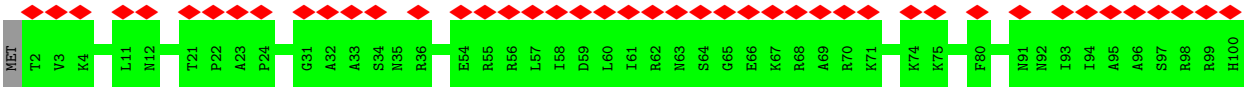




• Molecule 35: 60S ribosomal protein L36-A

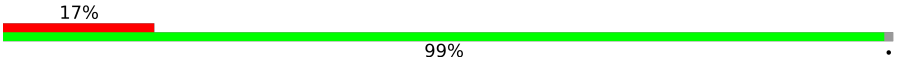
Chain i:

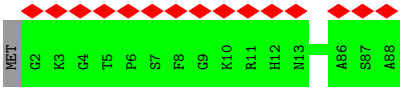




• Molecule 36: 60S ribosomal protein L37-A

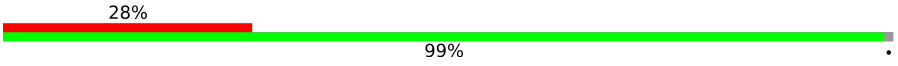
Chain j:

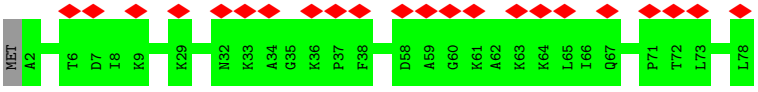




• Molecule 37: 60S ribosomal protein L38

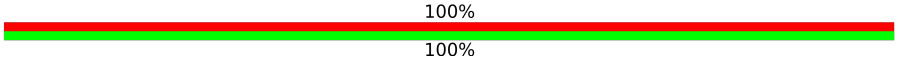
Chain k:

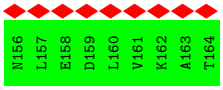




• Molecule 38: Nucleolar GTP-binding protein 2

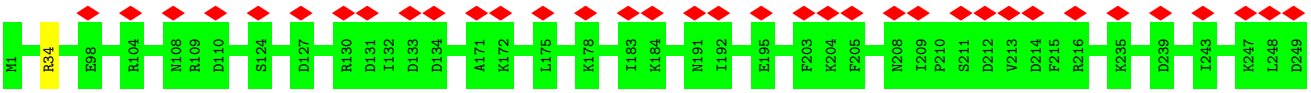
Chain m:

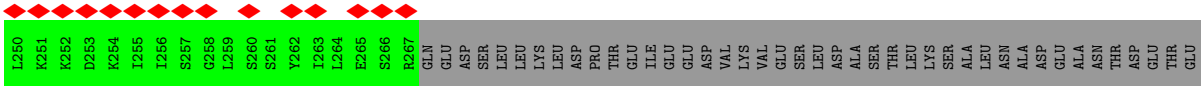


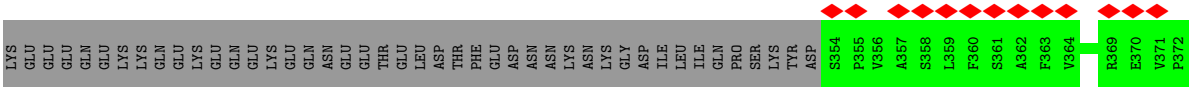


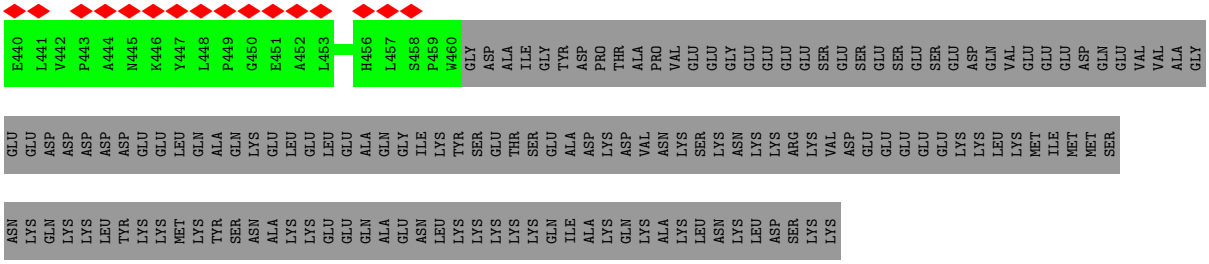
• Molecule 39: Pescadillo homolog

Chain n:



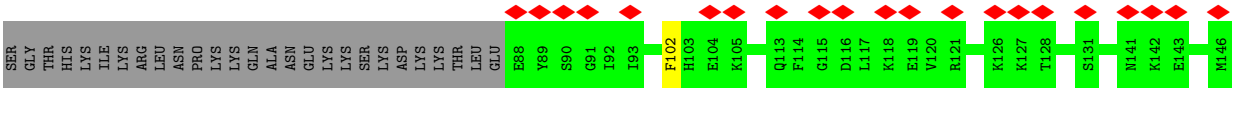


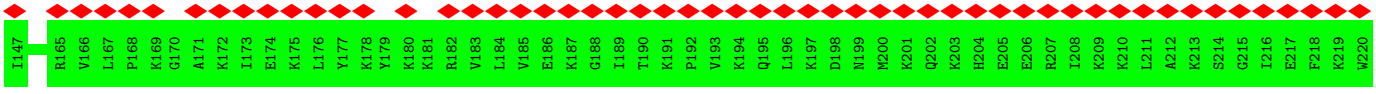




• Molecule 40: Ribosome biogenesis protein 15

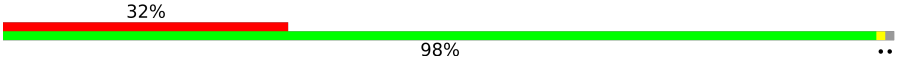
Chain o:

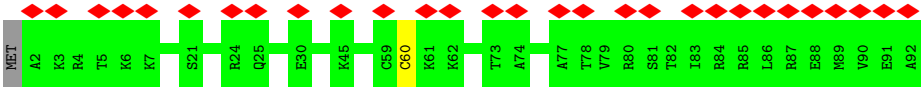




• Molecule 41: 60S ribosomal protein L43-A

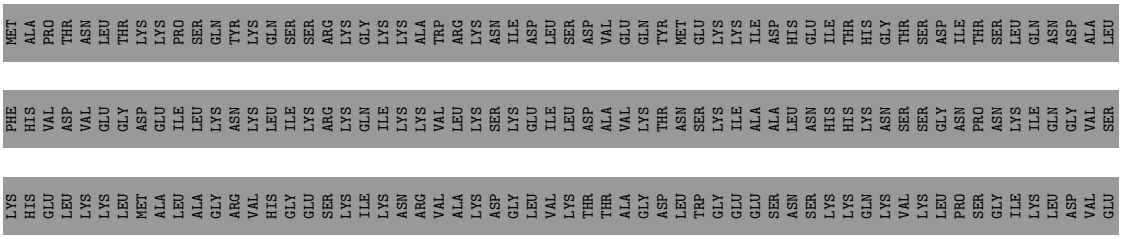
Chain p:

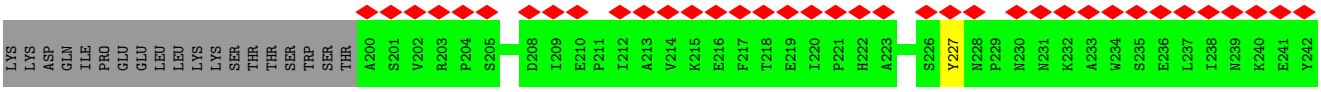


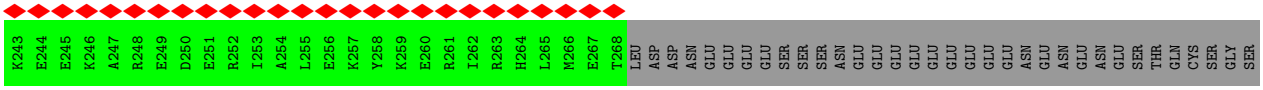


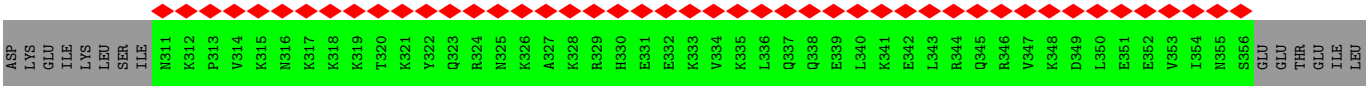
• Molecule 42: Ribosome biogenesis protein NOP53

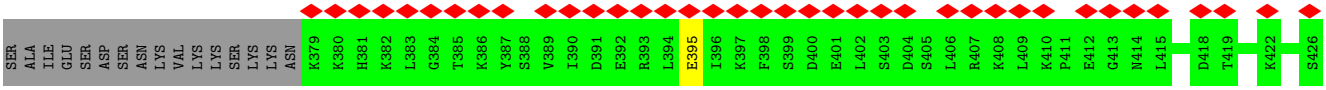
Chain q:

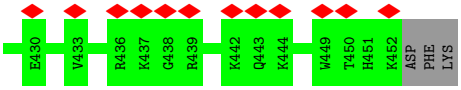






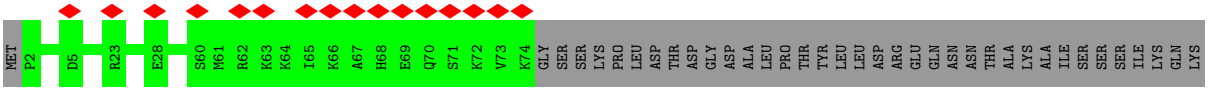


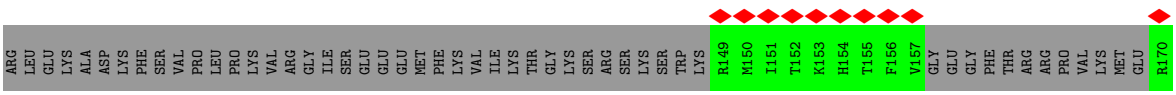


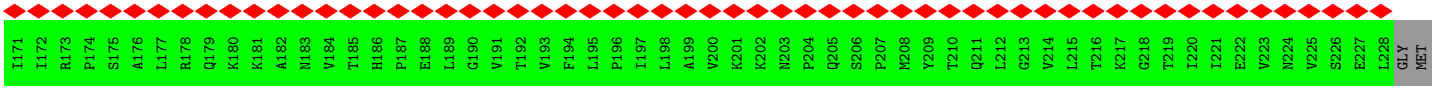


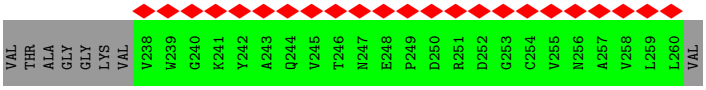
• Molecule 43: Ribosome biogenesis protein NSA2

Chain r:



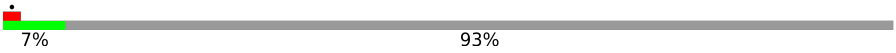


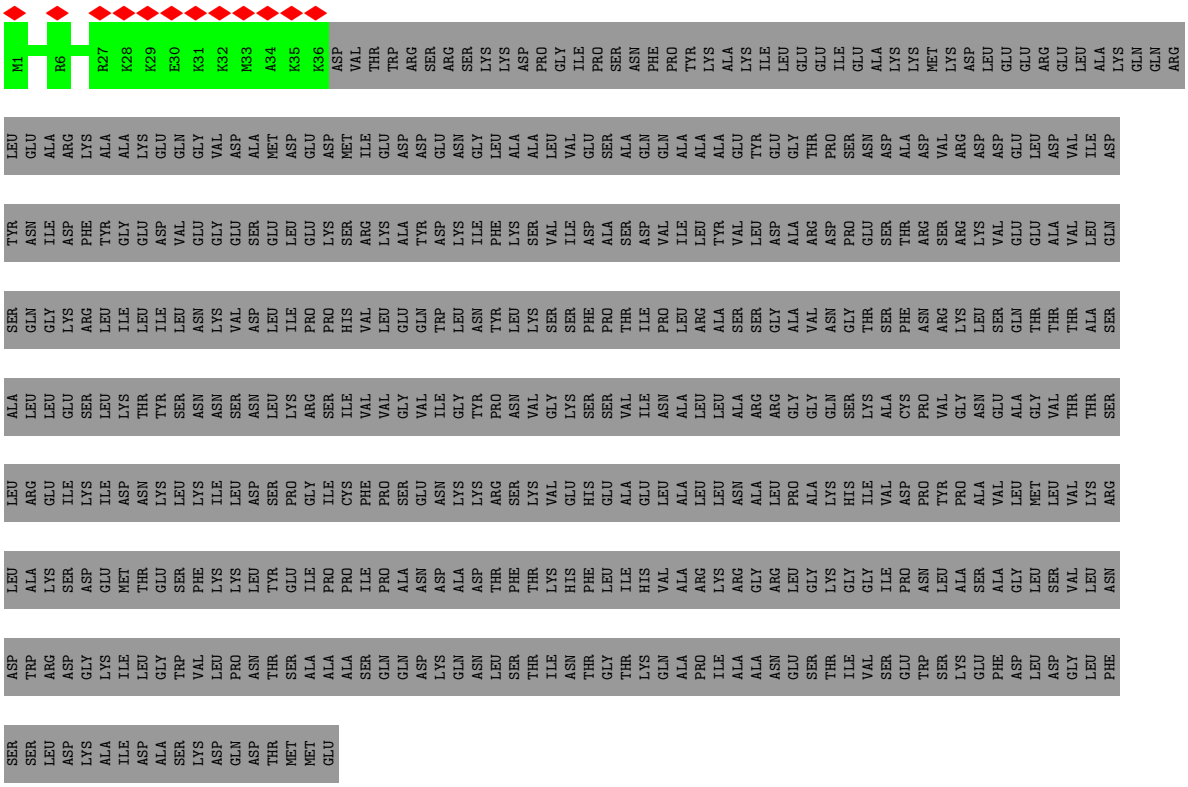




• Molecule 44: Nuclear GTP-binding protein NUG1

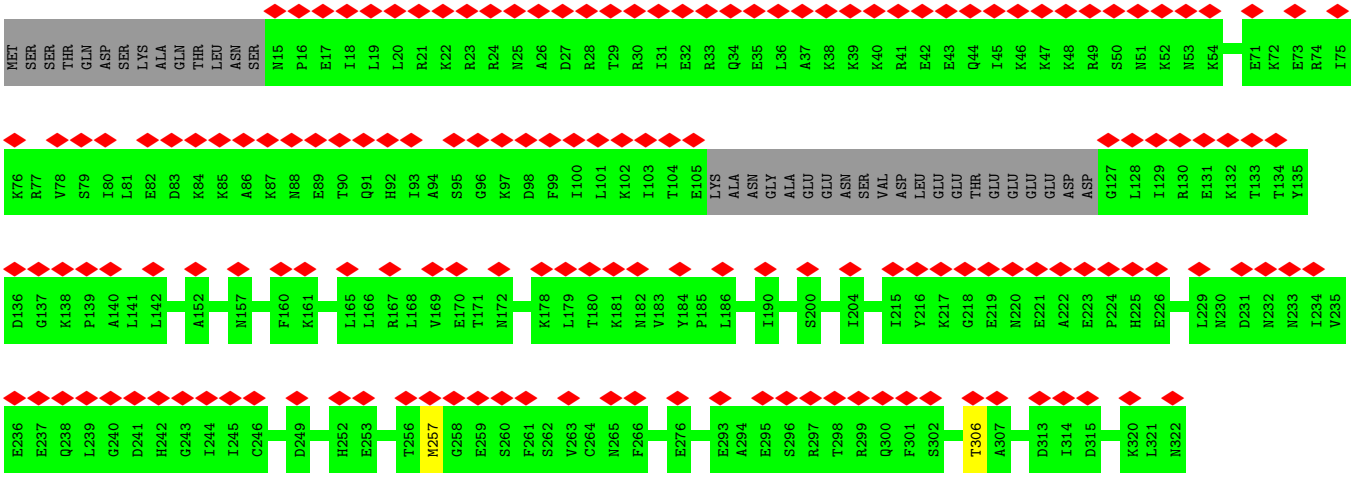
Chain s:





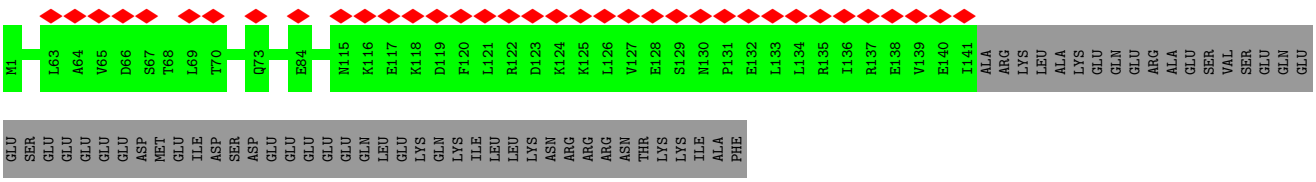
• Molecule 45: Ribosome biogenesis protein RLP7

Chain t:



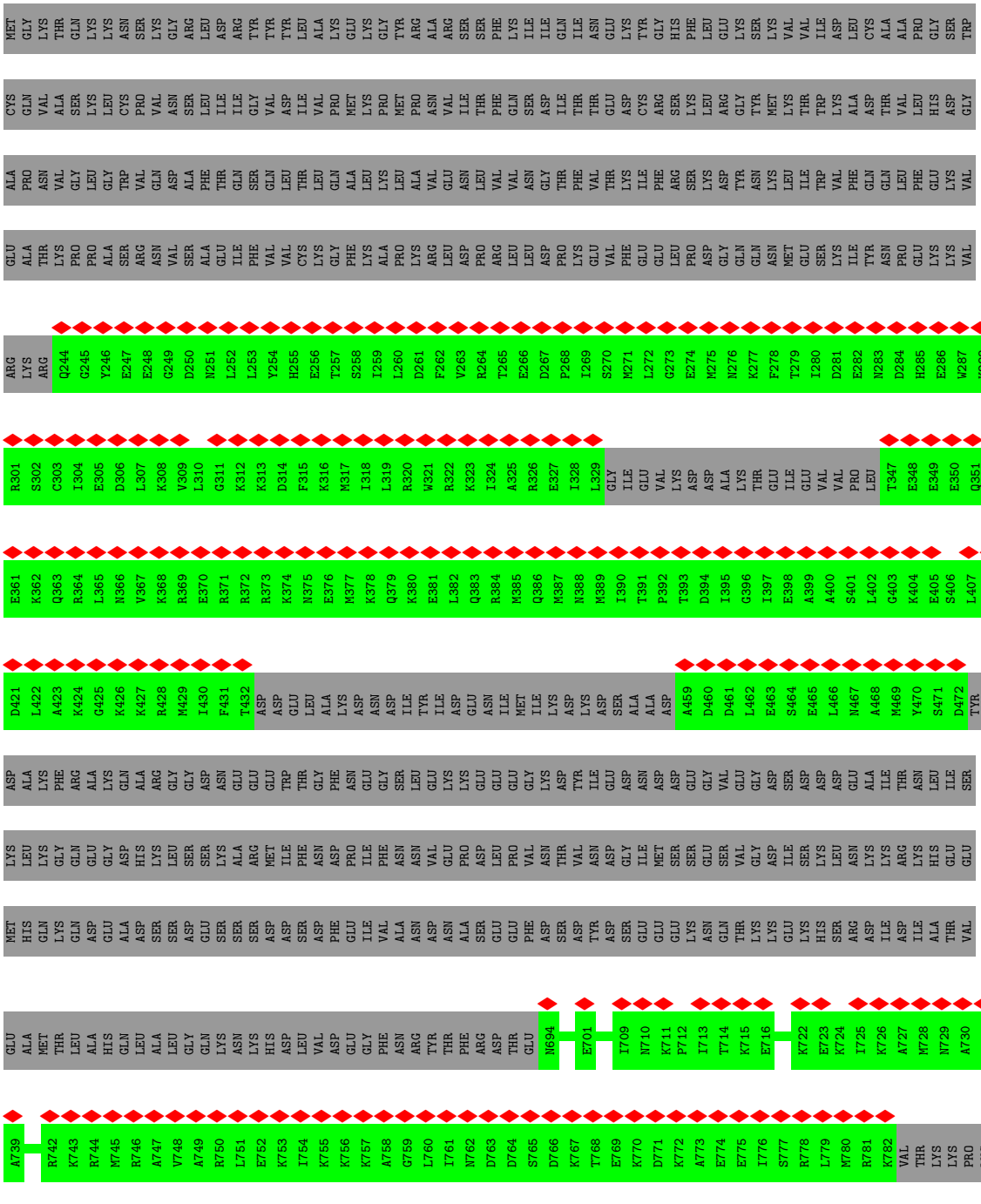
• Molecule 46: Ribosome biogenesis protein RLP24

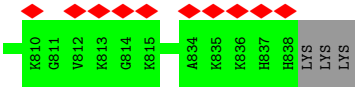
Chain u:



• Molecule 47: 27S pre-rRNA (guanosine(2922)-2'-O)-methyltransferase

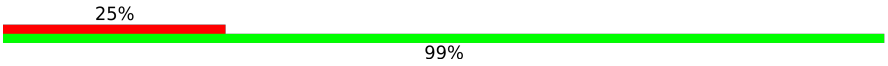
Chain w:

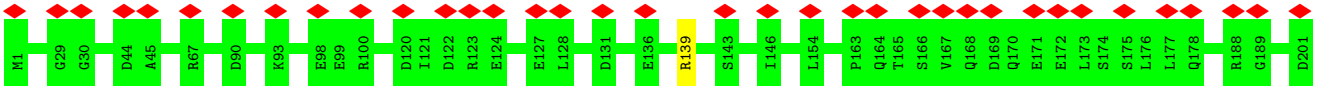


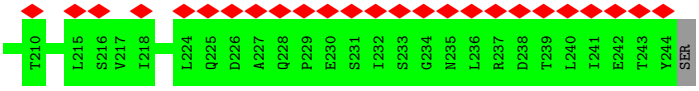


• Molecule 48: Eukaryotic translation initiation factor 6

Chain y:

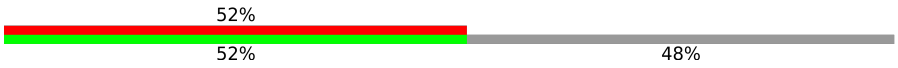


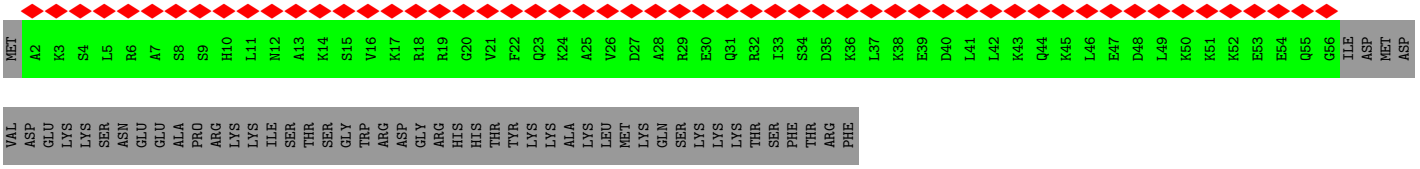




• Molecule 49: UPF0642 protein YBL028C

Chain z:





4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	83000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	1.2	Depositor
Minimum defocus (nm)	900	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.319	Depositor
Minimum map value	-0.169	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.0284	Depositor
Map size (Å)	411.53998, 411.53998, 411.53998	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.02885, 1.02885, 1.02885	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, ZN

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|>5$	RMSZ	#$\|Z\|>5$
1	1	0.46	0/65173	0.83	16/101591 (0.0%)
2	2	0.54	0/3746	0.84	0/5832
3	6	0.31	0/1390	0.82	0/2156
4	A	0.27	0/1382	0.56	0/1860
5	B	0.30	0/2755	0.54	0/3700
6	C	0.29	0/2801	0.53	0/3792
7	E	0.28	0/1260	0.52	0/1694
8	F	0.31	0/1821	0.51	0/2451
9	G	0.29	0/1496	0.50	0/2023
10	H	0.29	0/1539	0.51	0/2073
11	K	0.26	0/2098	0.48	0/2830
12	L	0.28	0/1483	0.57	0/1991
13	M	0.28	0/1074	0.52	0/1446
14	N	0.32	0/1637	0.62	0/2189
15	O	0.31	0/1585	0.52	0/2128
16	P	0.29	0/1360	0.55	0/1824
17	Q	0.28	0/1149	0.54	0/1550
18	R	0.27	0/1275	0.54	0/1702
19	S	0.30	0/1473	0.52	0/1980
20	T	0.25	0/434	0.50	0/575
21	U	0.28	0/861	0.49	0/1167
22	V	0.30	0/1018	0.54	0/1369
23	W	0.26	0/1902	0.51	0/2564
24	X	0.30	0/1097	0.52	0/1476
25	Y	0.30	0/1004	0.55	0/1341
26	Z	0.30	0/1113	0.48	0/1490
27	a	0.27	0/747	0.48	0/1008
28	b	0.27	0/4508	0.50	0/6068
29	c	0.29	0/751	0.48	0/1008
30	d	0.29	0/887	0.54	0/1191
31	e	0.29	0/1033	0.54	0/1383
32	f	0.32	0/868	0.56	0/1168

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
33	g	0.30	0/891	0.57	0/1191
34	h	0.28	0/978	0.51	0/1301
35	i	0.26	0/778	0.57	0/1034
36	j	0.31	0/696	0.60	0/923
37	k	0.27	0/618	0.52	0/826
38	m	0.26	0/68	0.54	0/91
39	n	0.28	0/3071	0.50	0/4147
40	o	0.27	0/1129	0.51	0/1502
41	p	0.29	0/701	0.56	0/934
42	q	0.26	0/1610	0.51	0/2143
43	r	0.26	0/1362	0.52	0/1818
44	s	0.26	0/301	0.57	0/386
45	t	0.27	0/2333	0.52	0/3128
46	u	0.29	0/1213	0.56	0/1614
47	w	0.26	0/2633	0.49	0/3493
48	y	0.27	0/1872	0.53	0/2548
49	z	0.26	0/445	0.49	0/585
All	All	0.39	0/133419	0.71	16/194284 (0.0%)

There are no bond length outliers.

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	1	406	G	O4'-C1'-N9	8.52	115.01	108.20
1	1	1199	C	C2-N1-C1'	6.97	126.47	118.80
1	1	2861	U	C2-N1-C1'	6.42	125.41	117.70
1	1	1199	C	C6-N1-C1'	-6.32	113.21	120.80
1	1	3092	C	C2-N1-C1'	6.27	125.70	118.80

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	A	174/254 (68%)	164 (94%)	10 (6%)	0	100	100
5	B	336/387 (87%)	328 (98%)	8 (2%)	0	100	100
6	C	359/362 (99%)	351 (98%)	8 (2%)	0	100	100
7	E	152/176 (86%)	149 (98%)	3 (2%)	0	100	100
8	F	220/244 (90%)	215 (98%)	5 (2%)	0	100	100
9	G	181/256 (71%)	179 (99%)	2 (1%)	0	100	100
10	H	189/191 (99%)	185 (98%)	4 (2%)	0	100	100
11	K	252/376 (67%)	244 (97%)	8 (3%)	0	100	100
12	L	180/199 (90%)	176 (98%)	4 (2%)	0	100	100
13	M	135/138 (98%)	132 (98%)	3 (2%)	0	100	100
14	N	183/204 (90%)	176 (96%)	7 (4%)	0	100	100
15	O	195/199 (98%)	194 (100%)	1 (0%)	0	100	100
16	P	164/184 (89%)	157 (96%)	7 (4%)	0	100	100
17	Q	144/186 (77%)	140 (97%)	4 (3%)	0	100	100
18	R	154/189 (82%)	152 (99%)	2 (1%)	0	100	100
19	S	169/172 (98%)	162 (96%)	7 (4%)	0	100	100
20	T	49/160 (31%)	48 (98%)	1 (2%)	0	100	100
21	U	104/121 (86%)	96 (92%)	8 (8%)	0	100	100
22	V	134/137 (98%)	128 (96%)	6 (4%)	0	100	100
23	W	230/236 (98%)	223 (97%)	7 (3%)	0	100	100
24	X	136/142 (96%)	133 (98%)	3 (2%)	0	100	100
25	Y	124/127 (98%)	124 (100%)	0	0	100	100
26	Z	132/136 (97%)	130 (98%)	2 (2%)	0	100	100
27	a	90/149 (60%)	83 (92%)	7 (8%)	0	100	100
28	b	542/647 (84%)	517 (95%)	25 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
29	c	95/105 (90%)	94 (99%)	1 (1%)	0	100	100
30	d	105/113 (93%)	104 (99%)	1 (1%)	0	100	100
31	e	124/130 (95%)	121 (98%)	3 (2%)	0	100	100
32	f	104/107 (97%)	103 (99%)	1 (1%)	0	100	100
33	g	110/121 (91%)	108 (98%)	2 (2%)	0	100	100
34	h	117/120 (98%)	115 (98%)	2 (2%)	0	100	100
35	i	97/100 (97%)	95 (98%)	2 (2%)	0	100	100
36	j	85/88 (97%)	82 (96%)	3 (4%)	0	100	100
37	k	75/78 (96%)	74 (99%)	1 (1%)	0	100	100
38	m	7/9 (78%)	7 (100%)	0	0	100	100
39	n	362/605 (60%)	349 (96%)	13 (4%)	0	100	100
40	o	131/220 (60%)	119 (91%)	12 (9%)	0	100	100
41	p	89/92 (97%)	84 (94%)	5 (6%)	0	100	100
42	q	183/455 (40%)	174 (95%)	9 (5%)	0	100	100
43	r	156/261 (60%)	150 (96%)	6 (4%)	0	100	100
44	s	34/520 (6%)	34 (100%)	0	0	100	100
45	t	283/322 (88%)	274 (97%)	9 (3%)	0	100	100
46	u	139/199 (70%)	137 (99%)	2 (1%)	0	100	100
47	w	311/841 (37%)	300 (96%)	11 (4%)	0	100	100
48	y	242/245 (99%)	232 (96%)	10 (4%)	0	100	100
49	z	53/106 (50%)	53 (100%)	0	0	100	100
All	All	7630/10409 (73%)	7395 (97%)	235 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	A	138/196 (70%)	138 (100%)	0	100	100
5	B	284/323 (88%)	283 (100%)	1 (0%)	91	93
6	C	288/289 (100%)	288 (100%)	0	100	100
7	E	134/153 (88%)	134 (100%)	0	100	100
8	F	186/205 (91%)	185 (100%)	1 (0%)	88	92
9	G	155/208 (74%)	155 (100%)	0	100	100
10	H	171/171 (100%)	171 (100%)	0	100	100
11	K	236/346 (68%)	236 (100%)	0	100	100
12	L	144/159 (91%)	144 (100%)	0	100	100
13	M	108/109 (99%)	108 (100%)	0	100	100
14	N	163/176 (93%)	162 (99%)	1 (1%)	86	90
15	O	160/162 (99%)	160 (100%)	0	100	100
16	P	137/146 (94%)	137 (100%)	0	100	100
17	Q	121/151 (80%)	121 (100%)	0	100	100
18	R	129/154 (84%)	129 (100%)	0	100	100
19	S	155/156 (99%)	154 (99%)	1 (1%)	86	90
20	T	45/137 (33%)	44 (98%)	1 (2%)	52	70
21	U	93/107 (87%)	92 (99%)	1 (1%)	73	84
22	V	104/105 (99%)	104 (100%)	0	100	100
23	W	209/213 (98%)	207 (99%)	2 (1%)	76	85
24	X	115/118 (98%)	115 (100%)	0	100	100
25	Y	109/110 (99%)	108 (99%)	1 (1%)	78	87
26	Z	115/116 (99%)	115 (100%)	0	100	100
27	a	76/119 (64%)	76 (100%)	0	100	100
28	b	490/573 (86%)	487 (99%)	3 (1%)	86	90
29	c	81/88 (92%)	80 (99%)	1 (1%)	71	82
30	d	94/97 (97%)	94 (100%)	0	100	100
31	e	108/111 (97%)	108 (100%)	0	100	100
32	f	90/91 (99%)	90 (100%)	0	100	100
33	g	95/103 (92%)	95 (100%)	0	100	100
34	h	104/105 (99%)	104 (100%)	0	100	100
35	i	81/82 (99%)	81 (100%)	0	100	100

Continued on next page...

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
36	j	70/71 (99%)	70 (100%)	0	100 100
37	k	68/69 (99%)	68 (100%)	0	100 100
38	m	8/8 (100%)	8 (100%)	0	100 100
39	n	331/548 (60%)	330 (100%)	1 (0%)	92 95
40	o	118/199 (59%)	117 (99%)	1 (1%)	81 88
41	p	71/72 (99%)	70 (99%)	1 (1%)	67 79
42	q	177/420 (42%)	175 (99%)	2 (1%)	73 84
43	r	146/229 (64%)	146 (100%)	0	100 100
44	s	32/445 (7%)	32 (100%)	0	100 100
45	t	256/287 (89%)	254 (99%)	2 (1%)	81 88
46	u	126/180 (70%)	126 (100%)	0	100 100
47	w	282/745 (38%)	282 (100%)	0	100 100
48	y	210/211 (100%)	209 (100%)	1 (0%)	88 92
49	z	48/95 (50%)	48 (100%)	0	100 100
All	All	6661/8958 (74%)	6640 (100%)	21 (0%)	92 95

5 of 21 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
40	o	102	PHE
42	q	395	GLU
48	y	139	ARG
45	t	257	MET
42	q	227	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
28	b	500	GLN
39	n	69	GLN
46	u	115	ASN
11	K	104	HIS
11	K	85	ASN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	2708/3396 (79%)	494 (18%)	7 (0%)
2	2	157/158 (99%)	23 (14%)	0
3	6	56/87 (64%)	21 (37%)	0
All	All	2921/3641 (80%)	538 (18%)	7 (0%)

5 of 538 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	5	G
1	1	14	U
1	1	16	A
1	1	40	A
1	1	42	C

5 of 7 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	956	U
1	1	1568	U
1	1	3269	U
1	1	3121	U
1	1	761	A

5.4 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 5 ligands modelled in this entry, 5 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

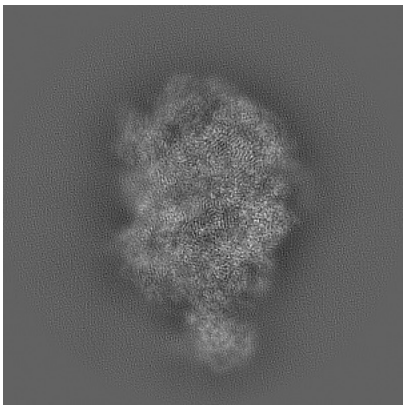
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-26259. These allow visual inspection of the internal detail of the map and identification of artifacts.

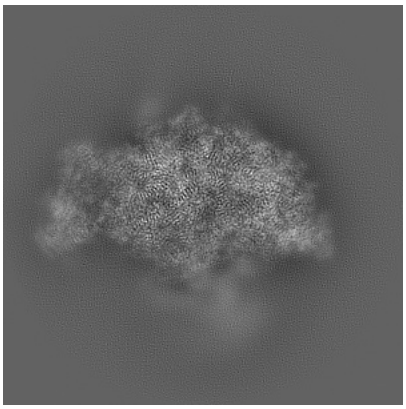
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

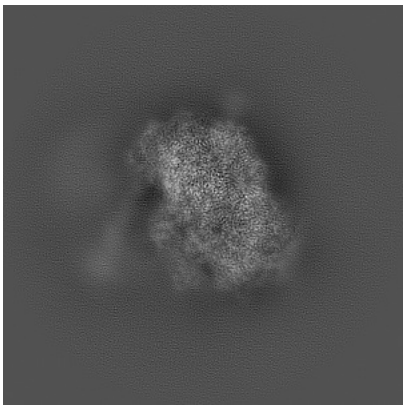
6.1.1 Primary map



X

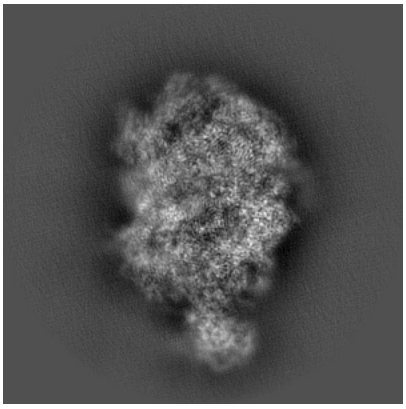


Y

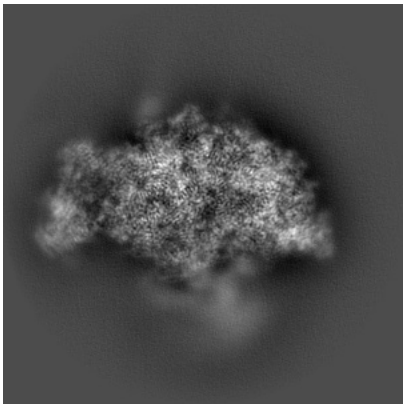


Z

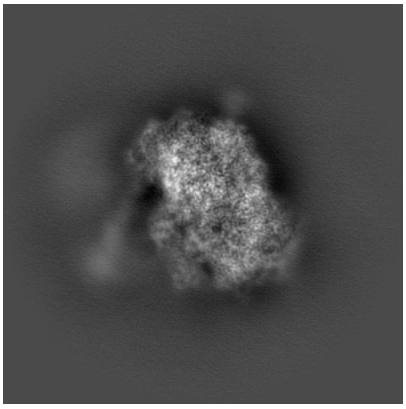
6.1.2 Raw map



X



Y

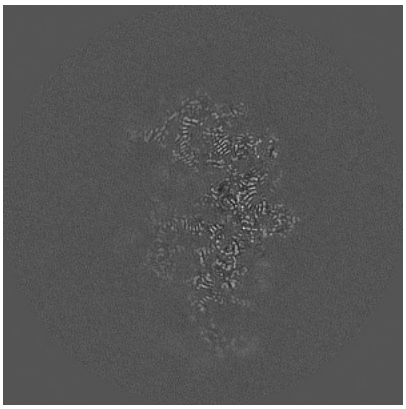


Z

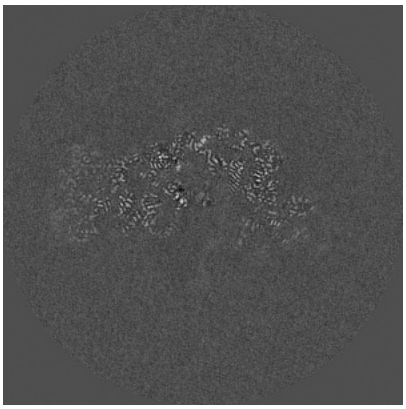
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

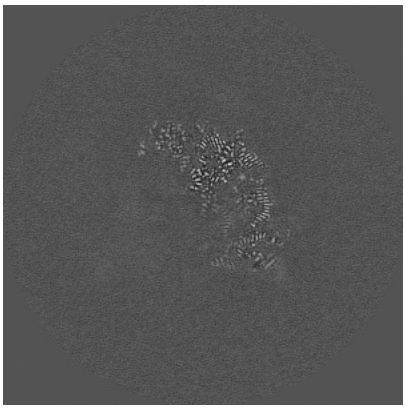
6.2.1 Primary map



X Index: 200

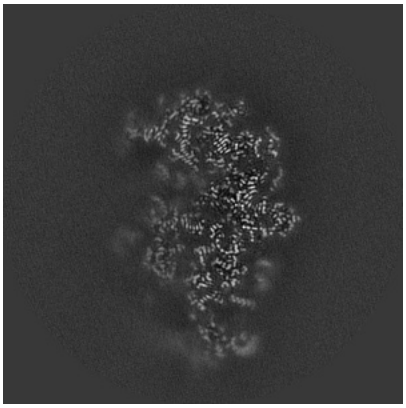


Y Index: 200

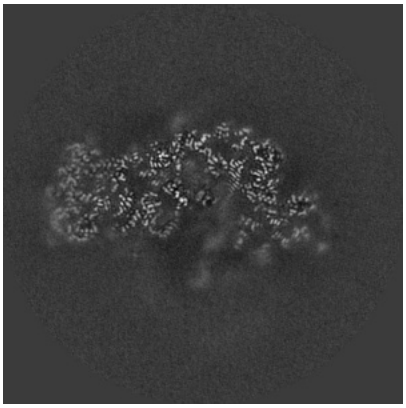


Z Index: 200

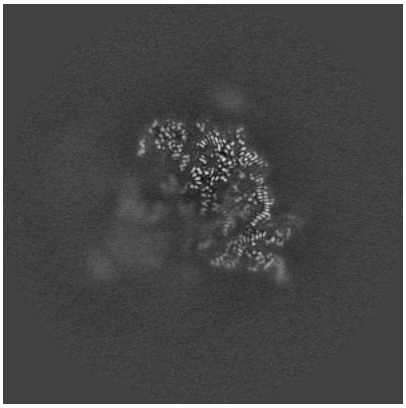
6.2.2 Raw map



X Index: 200



Y Index: 200

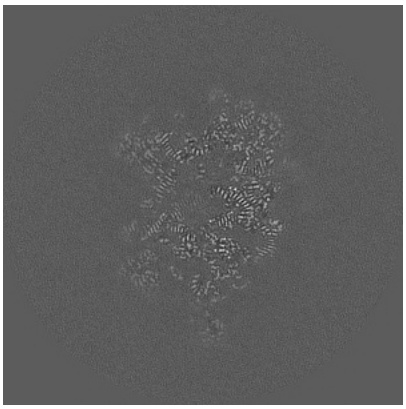


Z Index: 200

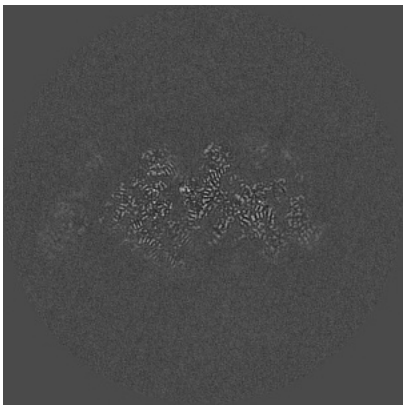
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

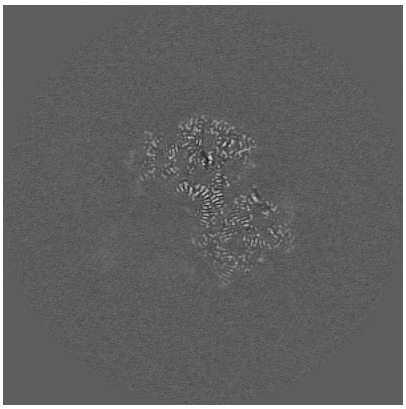
6.3.1 Primary map



X Index: 221

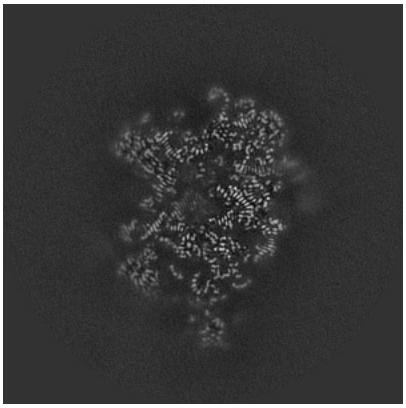


Y Index: 230

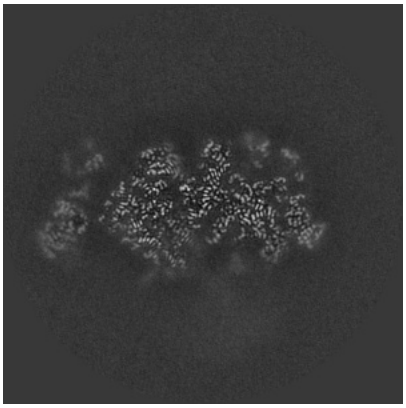


Z Index: 177

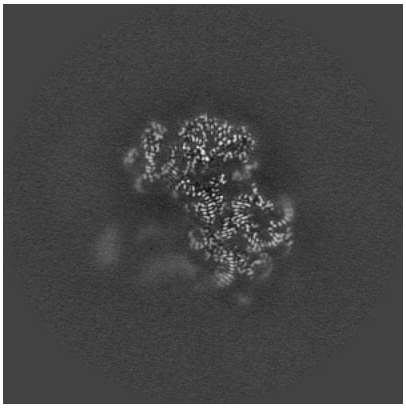
6.3.2 Raw map



X Index: 221



Y Index: 230

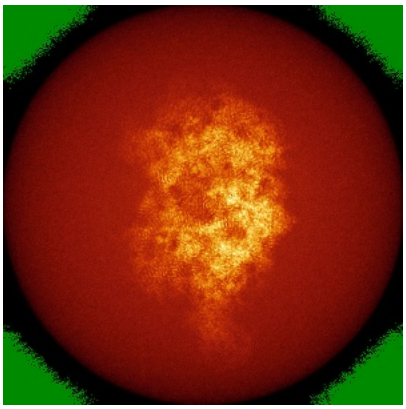


Z Index: 175

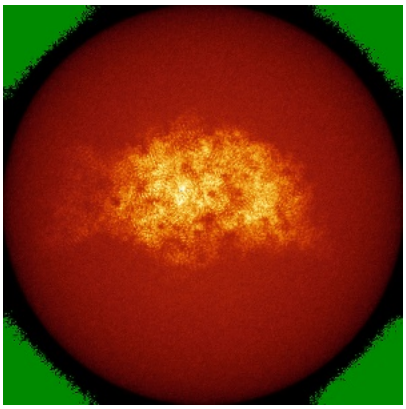
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

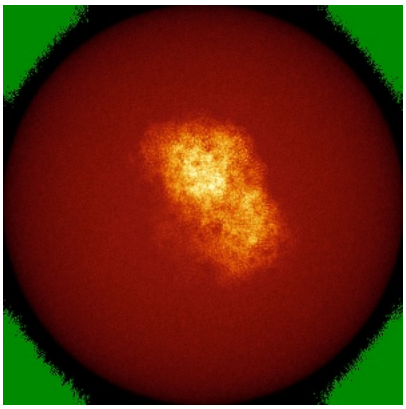
6.4.1 Primary map



X

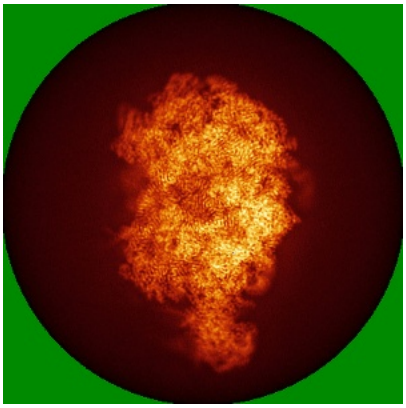


Y

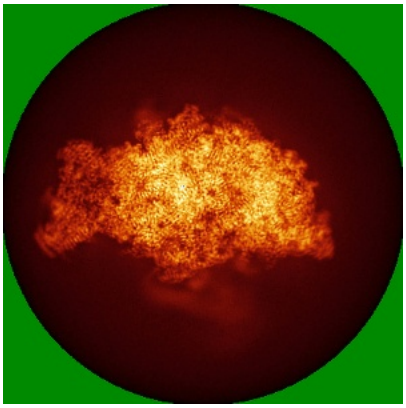


Z

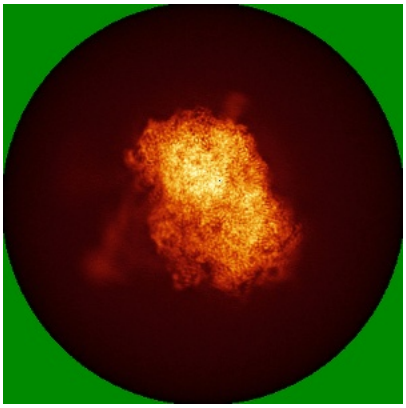
6.4.2 Raw map



X



Y



Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views (i)

6.5.1 Primary map

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.0284. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map

X Y Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

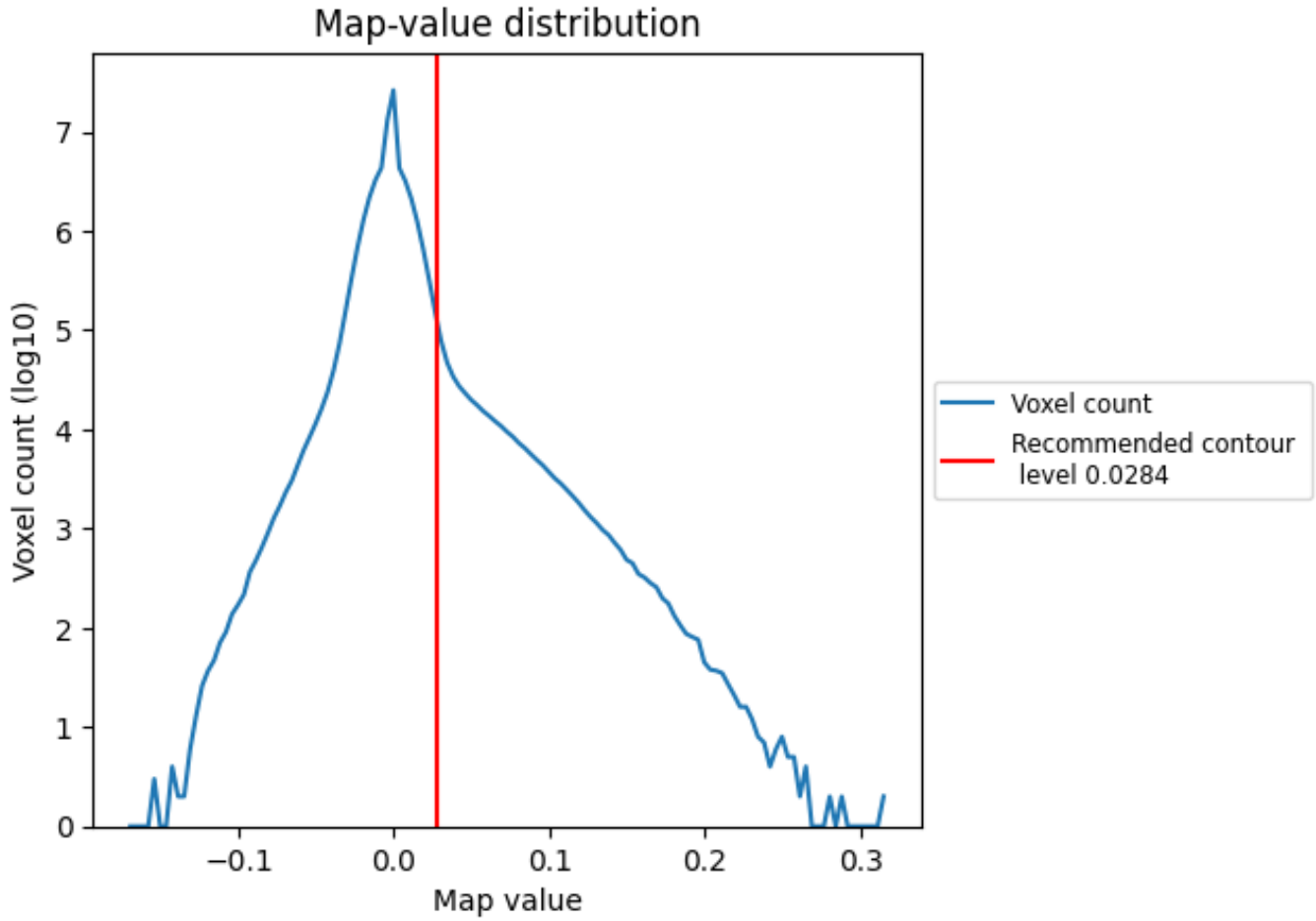
6.6 Mask visualisation (i)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis

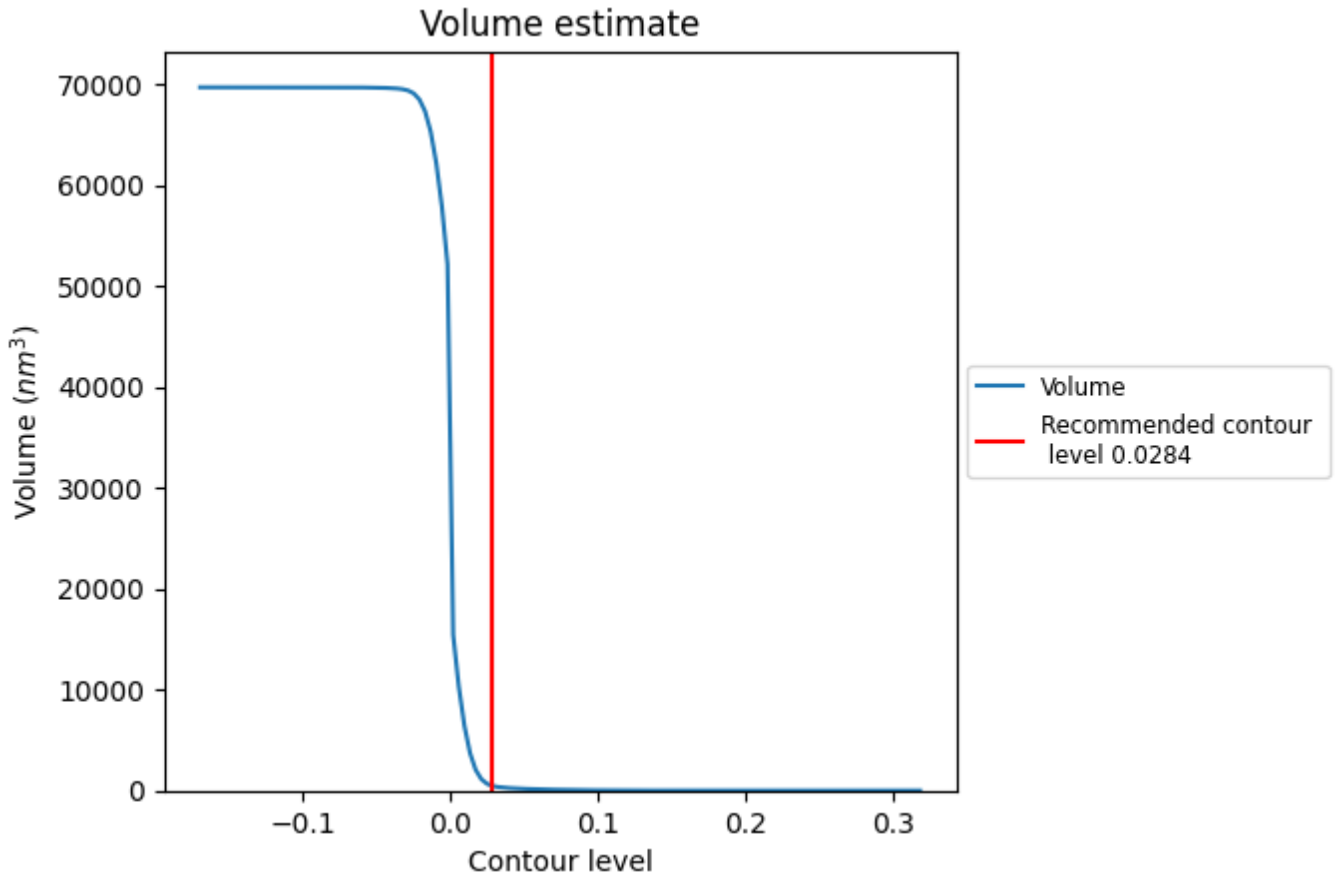
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

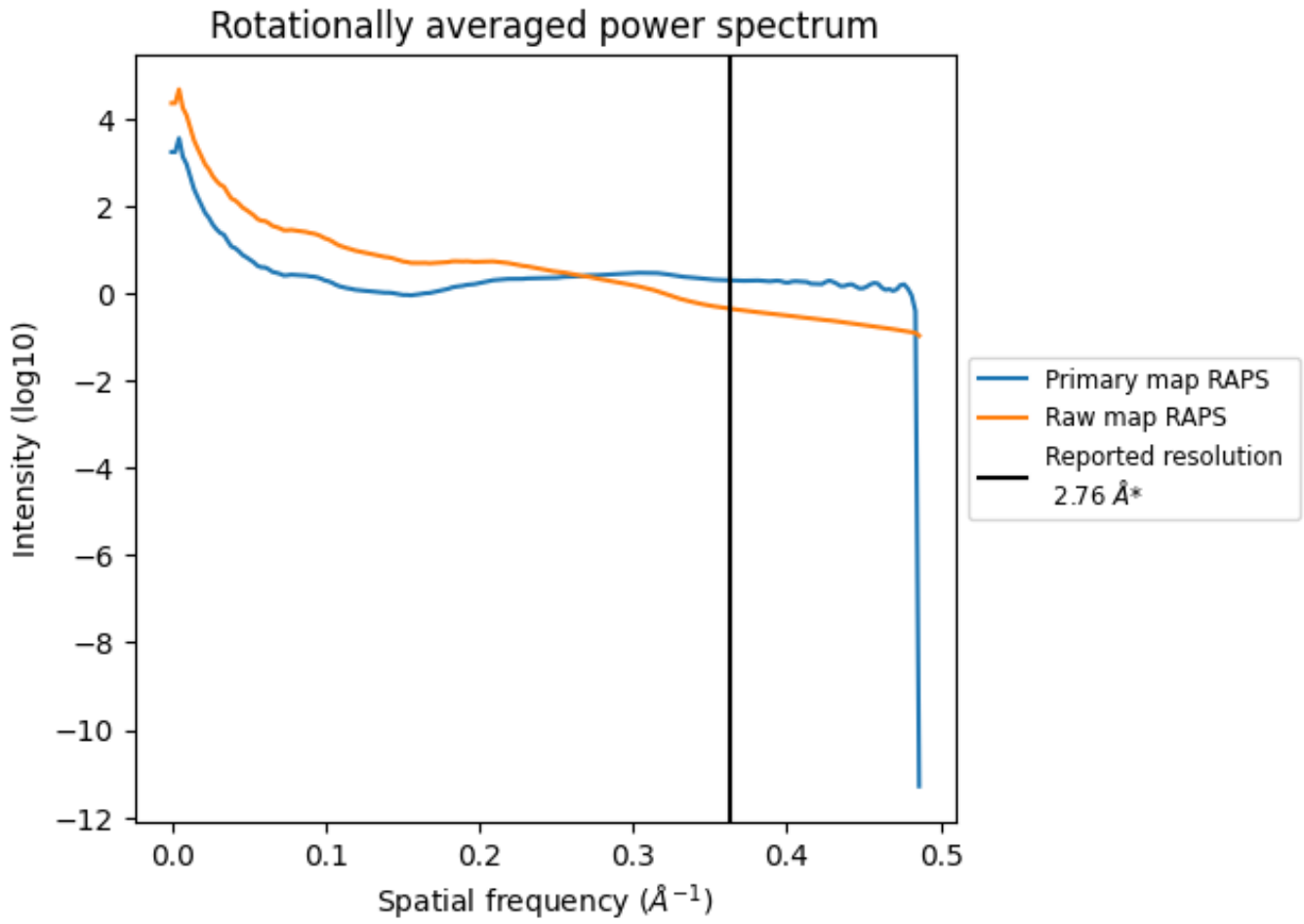
7.2 Volume estimate (i)



The volume at the recommended contour level is 490 nm^3; this corresponds to an approximate mass of 442 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum (i)

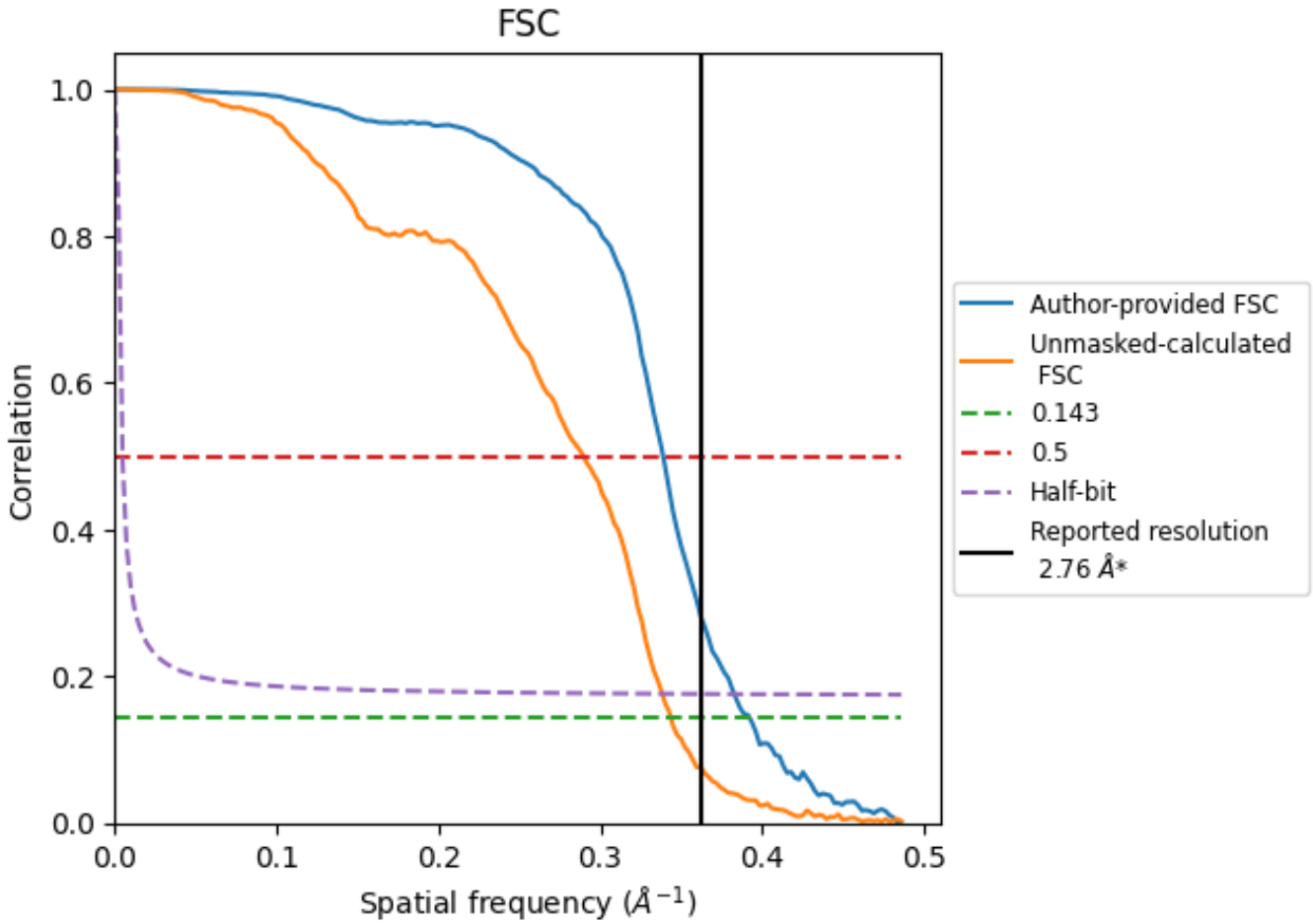


*Reported resolution corresponds to spatial frequency of 0.362 $Å^{-1}$

8 Fourier-Shell correlation

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC



*Reported resolution corresponds to spatial frequency of 0.362 Å^{-1}

8.2 Resolution estimates (i)

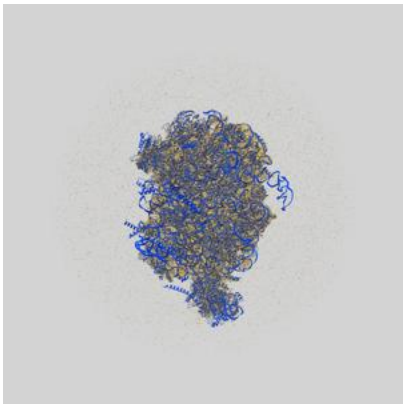
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.76	-	-
Author-provided FSC curve	2.55	2.95	2.61
Unmasked-calculated*	2.91	3.45	2.96

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

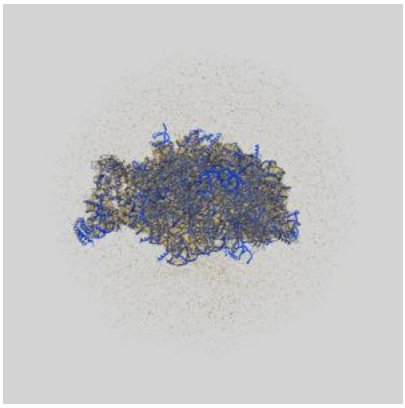
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-26259 and PDB model 7U0H. Per-residue inclusion information can be found in section 3 on page 13.

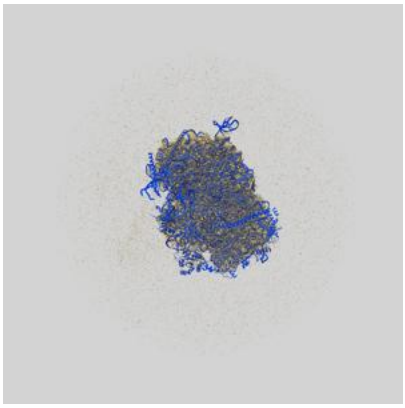
9.1 Map-model overlay



X



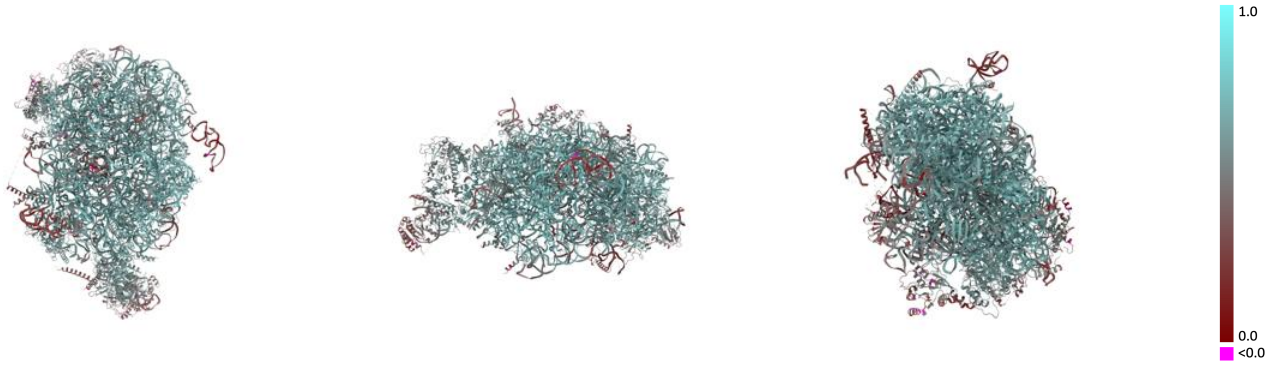
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0284 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

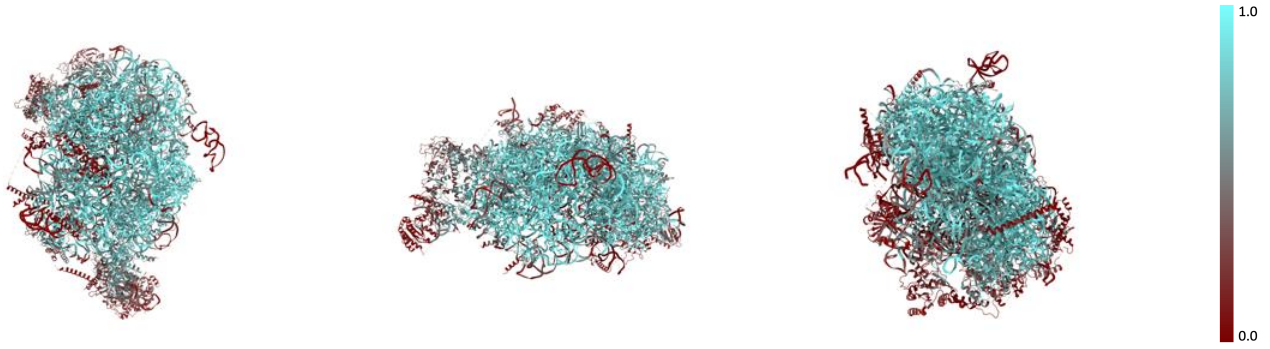
9.2 Q-score mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

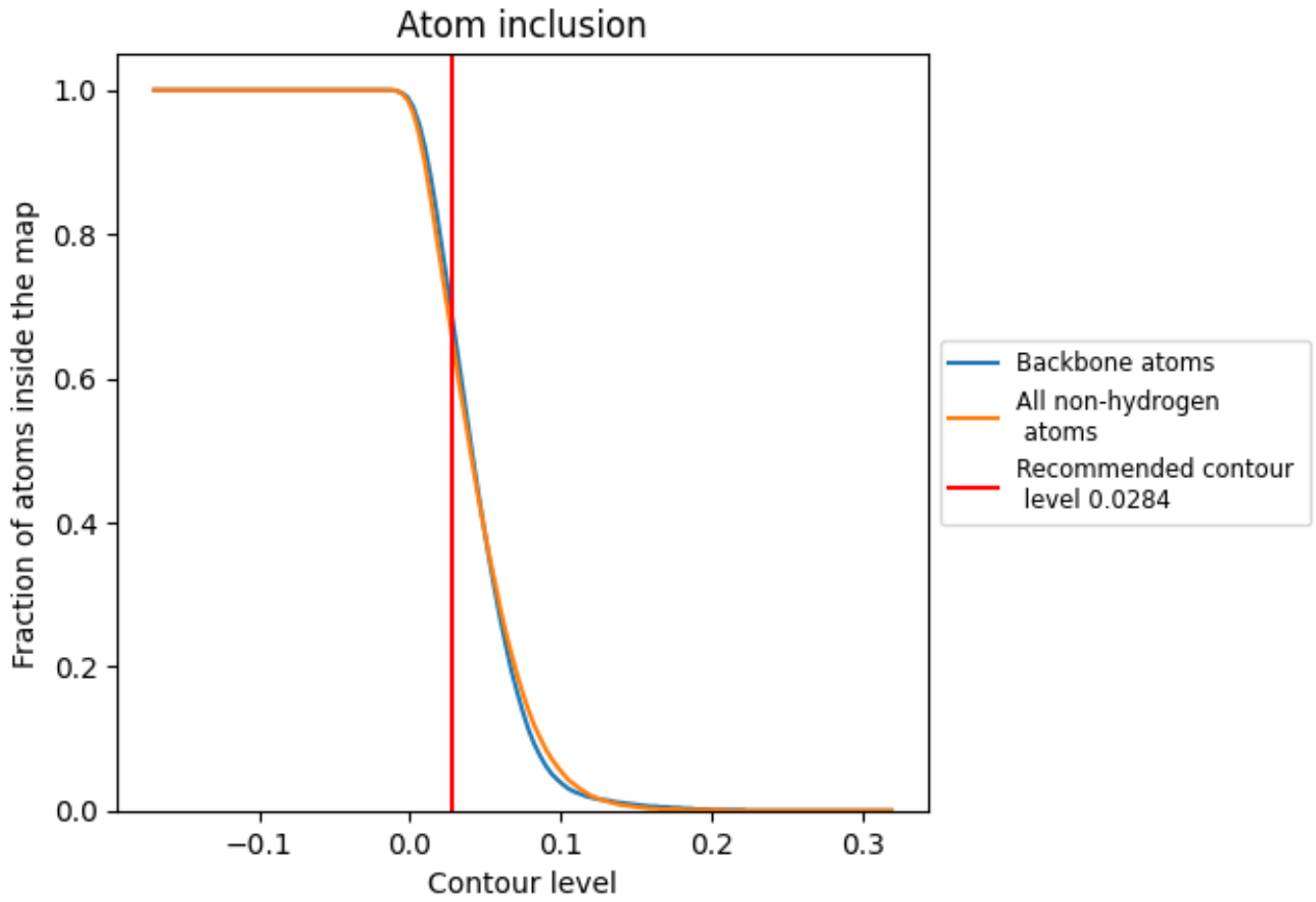
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0284).

9.4 Atom inclusion (i)



At the recommended contour level, 68% of all backbone atoms, 65% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.0284) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6490	0.5920
1	0.7110	0.5930
2	0.8590	0.6600
6	0.4190	0.4830
A	0.4290	0.5860
B	0.8750	0.6890
C	0.8510	0.6900
E	0.7400	0.6420
F	0.8200	0.6610
G	0.7100	0.6300
H	0.7010	0.6300
K	0.1600	0.4190
L	0.6990	0.6340
M	0.8000	0.6560
N	0.9000	0.7010
O	0.8820	0.6970
P	0.8120	0.6690
Q	0.8110	0.6560
R	0.7660	0.6530
S	0.6580	0.6090
T	0.0070	0.2750
U	0.4290	0.5210
V	0.6660	0.6340
W	0.1950	0.4470
X	0.8140	0.6770
Y	0.8470	0.6780
Z	0.5760	0.6080
a	0.7330	0.6410
b	0.2800	0.4730
c	0.4800	0.5610
d	0.7730	0.6540
e	0.8790	0.7000
f	0.9430	0.7160
g	0.7630	0.6470
h	0.8020	0.6690

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Chain	Atom inclusion	Q-score
i	0.4580	0.5640
j	0.7850	0.6630
k	0.5830	0.6040
m	0.0150	0.3200
n	0.5560	0.5840
o	0.3550	0.4660
p	0.5630	0.6110
q	0.1830	0.4720
r	0.3120	0.4980
s	0.4600	0.6020
t	0.3750	0.5230
u	0.6380	0.6200
w	0.1890	0.4580
y	0.5720	0.5700
z	0.0810	0.5060